```
                 GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:       May 27, 2005, 08:27:23 ; Search time 161 Seconds
                                       (without alignments)
                                       1054.583 Million cell updates/sec

Title:         US-10-734-510-7
Perfect score: 2325
Sequence:      1 MVSSAFAPSILLSLMSSLAL.........TYARENGQGDFAKCGFVPSE 439

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2105692 seqs, 386760381 residues
```

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

```
Database :   A_Geneseq_16Dec04:*
             1: geneseqp1980s:*
             2: geneseqp1990s:*
             3: geneseqp2000s:*
             4: geneseqp2001s:*
             5: geneseqp2002s:*
             6: geneseqp2003as:*
             7: geneseqp2003bs:*
             8: geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2325	100.0	439	2	AAW62858	Aaw62858 Peniophor
2	2325	100.0	439	2	AAW74484	Aaw74484 Peniophor
3	2325	100.0	439	2	AAY39895	Aay39895 P. lycii
4	2254	96.9	423	7	ADI66763	Adi66763 Peniophor
5	2248	96.7	423	7	ADI66783	Adi66783 Peniophor
6	2247	96.6	423	7	ADI66777	Adi66777 Peniophor
7	2246	96.6	423	7	ADI66835	Adi66835 Peniophor
8	2246	96.6	423	7	ADI66841	Adi66841 Peniophor
9	2246	96.6	423	7	ADI66837	Adi66837 Peniophor
10	2245	96.6	423	7	ADI66832	Adi66832 Peniophor
11	2245	96.6	423	7	ADI66845	Adi66845 Peniophor
12	2244	96.5	423	7	ADI66781	Adi66781 Peniophor
13	2244	96.5	423	7	ADI66778	Adi66778 Peniophor
14	2244	96.5	423	7	ADI66833	Adi66833 Peniophor
15	2243	96.5	423	7	ADI66843	Adi66843 Peniophor
16	2243	96.5	423	7	ADI66828	Adi66828 Peniophor
17	2242	96.4	423	7	ADI66836	Adi66836 Peniophor
18	2242	96.4	423	7	ADI66838	Adi66838 Peniophor
19	2241	96.4	423	7	ADI66782	Adi66782 Peniophor
20	2239	96.3	423	7	ADI66840	Adi66840 Peniophor
21	2238	96.3	419	3	AAY69573	Aay69573 Peniophor
22	2238	96.3	419	3	AAB20520	Aab20520 Peniophor
23	2238	96.3	419	8	ADL73086	Adl73086 Peniophor
24	2237	96.2	423	7	ADI66830	Adi66830 Peniophor
25	2237	96.2	423	7	ADI66822	Adi66822 Peniophor
26	2236	96.2	423	7	ADI66842	Adi66842 Peniophor
27	2235	96.1	423	7	ADI66839	Adi66839 Peniophor
28	2234	96.1	423	7	ADI66779	Adi66779 Peniophor
29	2233	96.0	423	7	ADI66844	Adi66844 Peniophor
30	2231	96.0	423	7	ADI66776	Adi66776 Peniophor
31	2231	96.0	423	7	ADI66829	Adi66829 Peniophor
32	2228	95.8	423	7	ADI66824	Adi66824 Peniophor
33	2227	95.8	423	7	ADI66780	Adi66780 Peniophor
34	2226	95.7	423	7	ADI66834	Adi66834 Peniophor
35	2225	95.7	430	7	ADI66825	Adi66825 Peniophor
36	2224	95.7	423	7	ADI66831	Adi66831 Peniophor
37	2223	95.6	423	7	ADI66820	Adi66820 Peniophor
38	2223	95.6	423	7	ADI66827	Adi66827 Peniophor
39	2222	95.6	423	7	ADI66823	Adi66823 Peniophor
40	2220	95.5	423	7	ADI66815	Adi66815 Peniophor
41	2219	95.4	423	7	ADI66819	Adi66819 Peniophor
42	2217	95.4	423	7	ADI66817	Adi66817 Peniophor
43	2216	95.3	423	7	ADI66821	Adi66821 Peniophor
44	2214	95.2	423	7	ADI66826	Adi66826 Peniophor
45	2212	95.1	423	7	ADI66818	Adi66818 Peniophor

ALIGNMENTS

```
RESULT 1
AAW62858
ID   AAW62858 standard; protein; 439 AA.
XX
AC   AAW62858;
XX
DT   17-OCT-2003  (revised)
DT   09-NOV-1998  (first entry)
XX
DE   Peniophora lycii 6-phytase.
XX
KW   6-Phytase; basidiomycetes; feed additive; feedstuff.
XX
OS   Peniophora lycii; strain CBS 686.96.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= Sig_peptide
FT   Protein         31..439
FT                   /label= Mat_protein
XX
PN   WO9828409-Al.
XX
PD   02-JUL-1998.
XX
PF   15-DEC-1997;   97WO-DK000568.
XX
PR   20-DEC-1996;   96DK-00001480.
PR   20-DEC-1996;   96DK-00001481.
PR   18-MAR-1997;   97DK-00000301.
PR   07-MAY-1997;   97DK-00000529.
PR   01-DEC-1997;   97DK-00001388.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Lassen SF, Bech L, Ohmann A, Breinholt J, Fuglsang CC;
XX
DR   WPI; 1998-377641/32.
DR   N-PSDB; AAV42331.
XX
PT   Phytase(s) from fungi of phylum Basidiomycota - useful as feed and food
PT   additives, e.g. to reduce phosphate content of manure and to improve
PT   digestibility.
XX
PS   Claim 25; Page 118-119; 197pp; English.
XX
CC   This polypeptide comprises a 6-phytase of the basidiomycete Peniophora
CC   lycii CBS 686.36. A cDNA clone (see AAV42331) encoding the enzyme was
```

CC obtained by expression cloning in yeast. The 6-phytase has been expressed
CC in Aspergillus oryzae. The recombinant enzyme is very stable at 40 degC
CC in the pH range 3-9, and 50-60% of activity is retained after 1 hr at 60-
CC 80 degC; this may be due to the enzyme's ability to refold following
CC thermal denaturation. The Peniophora phytase is more efficient than the
CC known Aspergillus phytase in releasing inorganic phosphate from corn. It
CC is essentially a 6-phytase, and at pH 3.5 is a phytase of hitherto
CC unknown type, i.e. a 3+6-phytase. The invention provides basidiomycete
CC phytases (see AAW42857-62), cloned DNA sequences (see AAV42330-35),
CC processes for preparing the phytases, and their use especially as food or
CC feed additives to improve digestibility. This novel subfamily of phytases
CC have a high degree of conserved regions (see AAW62843-56) in common.
CC Compared with known phytases, they show better heat stability or faster
CC release of phosphate from substrates, and may also show advantageous
CC position specificity and specific activity. They can be produced in
CC commercially useful quantities. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 439 AA;

Query Match   100.0%; Score 2325; DB 2; Length 439;
Best Local Similarity   100.0%;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy   61 TVTQVNLIQRHGARWPTSGARSRQAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TVTQVNLIQRHGARWPTSGARSRQAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy   181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy   241 CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy   301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy   361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCCGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCCGVDGVCELSAFVESQT 420

Qy   421 YARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||
Db   421 YARENGQGDFAKCGFVPSE 439

RESULT 2
AAW74484
ID AAW74484 standard; protein; 439 AA.
XX
AC AAW74484;
XX
DT 17-DEC-1998 (first entry)
XX
DE Peniophora phytase polypeptide.
XX
KW Phytase; inorganic phosphate; phytate; phytic acid.
XX
OS Peniophora lycii.
XX
PN WO9828408-A1.
XX

PD 02-JUL-1998.
XX
PF 10-DEC-1997; 97WO-DK000559.
XX
PR 20-DEC-1996; 96DK-00001481.
PR 07-MAY-1997; 97DK-00000529.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Lassen SF, Bech L, Fuglsang CC, Breinholt J, Ohmann A;
PI Ostergaard PR;
XX
DR WPI; 1998-467148/40.
DR N-PSDB; AAV41837.
XX
PT New isolated Peniophora lycii phytase - used in human food or animal
PT feed, for reducing phytate levels or improving protein availability or
PT bio:availability of minerals.
XX
PS Claim 1; Page 54-57; 82pp; English.
XX
CC The present sequence represents a polypeptide exhibiting phytase activity
CC encoded by a cDNA derived from Peniophora lycii. This protein has been
CC found to have superior properties to known phytases such as increased
CC heat stability or faster release of phytate. The polypeptide produced can
CC be used in e.g. liberating inorganic phosphate from phytate or phytic
CC acid, in human food or animal feed preparations or in additives for such
CC preparations
XX
SQ Sequence 439 AA;

Query Match   100.0%; Score 2325; DB 2; Length 439;
Best Local Similarity   100.0%;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy   61 TVTQVNLIQRHGARWPTSGARSRQAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TVTQVNLIQRHGARWPTSGARSRQAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy   181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy   241 CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy   301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy   361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCCGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCCGVDGVCELSAFVESQT 420

Qy   421 YARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||
Db   421 YARENGQGDFAKCGFVPSE 439

RESULT 3
AAY39895
ID AAY39895 standard; protein; 439 AA.
XX
AC AAY39895;

```
Qy  241 CPFDFTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVNELLARL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CPFDFTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVNELLARL 300

Qy  301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy  361 NRLWYDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NRLWYDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy  421 YARENGQGDFAKCGFVPSE 439
        |||||||||||||||||||
Db  421 YARENGQGDFAKCGFVPSE 439
```

```
RESULT 4
ADI66763
ID   ADI66763  standard; protein; 423 AA.
XX
AC   ADI66763;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase SEQ ID NO:2.
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion.
XX
OS   Peniophora lycii.
XX
XX
PN   WO2003066847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
DR   N-PSDB; ADI66762.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 1; SEQ ID NO 2; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed composition
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents the phytase used in the invention.
XX
SQ   Sequence 423 AA;

Query Match     96.9%;    Score 2254;  DB 7;  Length 423;
Best Local Similarity  100.0%;  Pred. No. 1.8e-217;
Matches  423;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 76
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 60

Qy   77 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGDMYTRY 136
        |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
XX
DT   27-AUG-2003  (revised)
DT   07-DEC-1999  (first entry)
XX
DE   P. lycii phytase protein sequence.
XX
KW   Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
KW   phytate level reduction; animal manure; food preparation; soy processing;
KW   inositol manufacture.
XX
OS   Peniophora lycii.
XX
PN   WO949022-A1.
XX
PD   30-SEP-1999.
XX
PF   22-MAR-1999;  99WO-DK000153.
XX
PR   23-MAR-1998;  98DK-00000407.
PR   19-JUN-1998;  98DK-00000806.
PR   18-SEP-1998;  98DK-00001176.
PR   22-JAN-1999;  99DK-00000091.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Svendsen A;
XX
DR   WPI; 1999-580444/49.
DR   N-PSDB; AAZ27412.
XX
PT   New variant phytase enzymes, used for liberating phosphorus from a
PT   phytase substrate, for reducing phytate levels in animal manure and in
PT   feed and food preparations.
XX
PS   Claim 1; Fig 6; 141pp; English.
XX
CC   This sequence represents the Peniophora lycii phytase sequence. The
CC   invention relates to variant phytase enzymes with specific amino acid
CC   substitutions for improved properties. The phytase variants can be used
CC   for liberating phosphorus from a phytase substrate. They can be used for
CC   reducing phytate levels in animal manure. They can be used in feed or
CC   food preparations. The phytase DNA can also be used to produce transgenic
CC   plants which can be used in feeds or foods. The phytase variants can also
CC   be used in soy processing and in the manufacture of inositol or
CC   derivatives. The phytase variants can have altered activities such as pH
CC   stability, temperature stability, pH profile, temperature profile,
CC   specific activity (in particularly in relation to pH and temperature),
CC   substrate specificity, substrate cleavage pattern, substrate binding,
CC   position specificity, the velocity and level of release of phosphate from
CC   corn, reaction rate, phytase degradation rate and end level of released
CC   phosphate reached. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 439 AA;

Query Match     100.0%;    Score 2325;  DB 2;  Length 439;
Best Local Similarity  100.0%;  Pred. No. 1.4e-224;
Matches  439;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy   61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy  121 GANQSHQTGDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GANQSHQTGDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy  181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
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Db     61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180
Qy    197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 240
Qy    257  LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300
Qy    317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360
Qy    377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420
Qy    437  PSE 439
           |||
Db    421  PSE 423
```

```
RESULT 5
ADI66783
ID   ADI66783 standard; protein; 423 AA.
XX
AC   ADI66783;
XX
DT   22-APR-2004  (first entry)
ZX
DE   Peniophora lycii phytase mutant (viii).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   Misc-difference  29
FT                    /label= Wild-type D substituted by S
XX
PN   WO2003066847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fugisang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;
```

```
Query Match             96.7%;   Score 2248;  DB 7;  Length 423;
Best Local Similarity   99.8%;   Pred. No. 7.4e-217;
Matches  422;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      1  SLALSTQFSFVAAQLPIPAQNTSNWGPYSPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  60
Qy     77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 120
Qy    137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180
Qy    197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 240
Qy    257  LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300
Qy    317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360
Qy    377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420
Qy    437  PSE 439
           |||
Db    421  PSE 423
```

```
RESULT 6
ADI66777
ID   ADI66777 standard; protein; 423 AA.
XX
AC   ADI66777;
XX
DT   22-APR-2004  (first entry)
ZX
DE   Peniophora lycii phytase mutant (ii).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   Misc-difference  29
FT                    /label= Wild-type D substituted by N
FT   Misc-difference  102
FT                    /note= "Wild-type L substituted by I"
XX
PN   WO2003066847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
```

```
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytae of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match          96.6%;     Score 2247;  DB 7;   Length 423;
Best Local Similarity 99.5%;    Pred. No. 9.3e-217;
Matches 421;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPPVEPYRAAPPEGCTVTQVNLIQRHGARWP  76
          ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db     1  SLALSTQFSFVAAQLPIPAQNTSNWGPYNPFPPVEPYRAAPPEGCTVTQVNLIQRHGARWP  60

Qy    77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLPPFGANQSHQTGTDMYTRY  136
          ||||||||||||||||||||||||||||||||||||||:  |||||||||||||||||||
Db    61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLIPFGANQSHQTGTDMYTRY  120

Qy   137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  196
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  180

Qy   197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFFDTLSSGNASPFCD  256
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDTLTLMDMCPFFDTLSSGNASPFCD  240

Qy   257  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  300

Qy   317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  360

Qy   377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  420

Qy  .437  PSE 439
          |||
Db   421  PSE 423

- RESULT 7
ADI66835
ID   ADI66835 standard; protein; 423 AA.
XX
AC   ADI66835;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase mutant (1x).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
```

```
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   Misc-difference  218
FT                    /label= Wild-type A substituted by T
FT   Misc-difference  334
FT                    /note= "Wild-type A substituted by G"
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytae of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match          96.6%;     Score 2246;  DB 7;   Length 423;
Best Local Similarity 99.5%;    Pred. No. 1.2e-216;
Matches 421;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy    17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPPVEPYAAPPEGCTVTQVNLIQRHGARWP  60

Qy    77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  136
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  120

Qy   137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  196
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  180

Qy   197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFFDTLSSGNASPFCD  256
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDTLTLMDMCPFFDTLSSGNASPFCD  240

Qy   257  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  300

Qy   317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  376
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNGTALDPLKPDENRLWVDSKLVPFSGHM  360

Qy   377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  420
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```
Qy  437 PSE 439
        |||
Db  421 PSE 423

RESULT 8
ADI66841
ID   ADI66841 standard; protein; 423 AA.
XX
AC   ADI66841;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase mutant (lxvi).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 330
FT                   /label= Wild-type R substituted by R
XX
PN   WO2003066847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match      96.6%;  Score 2246;  DB 7;  Length 423;
Best Local Similarity  99.8%;  Pred. No. 1.2e-216;
Matches  422;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 76
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 60

Qy   77 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 136
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 120

Qy  137 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180

Qy  197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTIMDMCPFDTLSSGNASPFCD 256
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTIMDMCPFDTLSSGNASPFCD 240

Qy  257 LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQYNRTLD 316
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQYNRTLD 300

Qy  317 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SDPATFPLNRTFYADFSHDNTMVPIFAALRLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

Qy  377 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420

Qy  437 PSE 439
         |||
Db  421 PSE 423

RESULT 9
ADI66837
ID   ADI66837 standard; protein; 423 AA.
XX
AC   ADI66837;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase mutant (lxii).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 324
FT                   /label= Wild-type P substituted by S
XX
PN   WO2003066847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;
```

```
Query Match           96.6%;   Score 2246;  DB 7;  Length 423;
Best Local Similarity 99.8%;   Pred. No. 1.2e-216;
Matches 422;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  60

Qy    77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  136
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  120

Qy   137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  180

Qy   197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  240

Qy   257  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  316
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  300

Qy   317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  SDPATFPLNRTFYADFSHDNTMVSIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  360

Qy   377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  436
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  420

Qy   437  PSE  439
          |||
Db   421  PSE  423

RESULT 10.
ADI66832
ID   ADI66832 standard; protein; 423 AA.
XX
AC   ADI66832;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase mutant (lvii)..
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference  69
FT                   /label= Wild-type V substituted by A
FT   Misc-difference  334
FT                   /note= "Wild-type A substituted by E"
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
```

```
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI6763.
XX
SQ   Sequence 423 AA;

Query Match           96.6%;   Score 2245;  DB 7;  Length 423;
Best Local Similarity 99.5%;   Pred. No. 1.5e-216;
Matches 421;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy    17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  60

Qy    77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  136
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TSGARSRQAAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  120

Qy   137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  180

Qy   197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  240

Qy   257  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  316
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LFTAEEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  300

Qy   317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  376
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNETALDPLKPDENRLWVDSKLVPFSGHM  360

Qy   377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  436
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV  420

Qy   437  PSE  439
          |||
Db   421  PSE  423

RESULT 11
ADI66845
ID   ADI66845 standard; protein; 423 AA.
XX
AC   ADI66845;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase mutant (lxx).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
```

```
FT   Misc-difference 350
FT        /label= Wild-type D substituted by V
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PR   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

. Query Match    96.6%;    Score 2245;   DB 7;   Length 423;
  Best Local Similarity   99.8%;   Pred. No. 1.5e-216;
  Matches  422;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  60

Qy   77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  136
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  120

Qy  137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  196
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  180

Qy  197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  256
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  240

Qy  257  LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  316
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD  300

Qy  317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM  376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVVVSKLVPFSGHM  360

Qy  377  TVEKLACSGKEAVRVLVNDAVQPLEFCCGVDGVCELSAFVESQTYARENGQGDFAKCGFV  436
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  TVEKLACSGKEAVRVLVNDAVQPLEFCCGVDGVCELSAFVESQTYARENGQGDFAKCGFV  420

Qy  437  PSE  439
            |||
Db  421  PSE  423

RESULT 12
```

```
ADI66781
ID   ADI66781 standard; protein; 423 AA.
XX
AC   ADI66781;
XX
DT   22-APR-2004 (first entry)
XX
DE   Peniophora lycii phytase mutant (vi).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 29
FT        /label= Wild-type D substituted by N
FT   Misc-difference 234
FT        /note= "Wild-type N substituted by S"
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match    96.5%;    Score 2244;   DB 7;   Length 423;
Best Local Similarity   99.5%;   Pred. No. 1.9e-216;
Matches  421;  Conservative   2;  Mismatches  2;  Indels  0;  Gaps  0;

Qy   17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  60

Qy   77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  136
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY  120

Qy  137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  196
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC  180

Qy  197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD  256
            |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db  181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGSASPFCD  240
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Qy   257 LFTABEYVSEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LFTABEYVSEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300

Qy   317 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

Qy   377 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420

Qy   437 PSE 439
         |||
Db   421 PSE 423
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RESULT 13
ADI66778
ID   ADI66778 standard; protein; 423 AA.
XX
AC   ADI66778;
XX
DT   22-APR-2004 (first entry)
XX
DE   Peniophora lycii phytase mutant (iii).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference   29
FT   /label= Wild-type D substituted by N
FT   Misc-difference   118
FT   /note= "Wild-type T substituted by A"
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match   96.5%; Score 2244; DB 7; Length 423;
Best Local Similarity   99.5%; Pred. No. 1.9e-216;

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Matches 421; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy    17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 76
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Db     1 SLALSTQFSFVAAQLPIPAQNTSNWGPYNPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 60

Qy    77 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 136
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :|
Db    61 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYARY 120

Qy   137 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180

Qy   197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 256
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Db   181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 240

Qy   257 LFTABEYVSEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LFTABEYVSEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300

Qy   317 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

Qy   377 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420

Qy   437 PSE 439
         |||
Db   421 PSE 423
```

RESULT 14
ADI66833
ID   ADI66833 standard; protein; 423 AA.
XX
AC   ADI66833;
XX
DT   22-APR-2004 (first entry)
XX
DE   Peniophora lycii phytase mutant (lviii).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference   99
FT   /label= Wild-type A substituted by D
FT   Misc-difference   398
FT   /note= "Wild-type A substituted by T"
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
XX
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating

```
FT                   /note= "Wild-type E substituted by A"
XX
PN   WO200306847-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-DK000067.
PR   08-FEB-2002; 2002DK-00000193.
PR   30-SEP-2002; 2002DK-00001449.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Matsui T, Fuglsang CC, Svendsen A,  Fukuyama S;
XX
DR   WPI; 2003-663595/62.
XX
PT   New phytase variants useful as animal feed additives and for treating
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match             96.5%;  Score 2243;  DB 7;  Length 423;
Best Local Similarity   99.5%;  Pred. No. 2.3e-216;
Matches   421;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 60

Qy         77 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVVKFGVADLLPFGANQSHQTGTDMYTRY 136
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Db         61 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVVKFGVADLLPFGANQSHQTGTDMYTRY 120

Qy        137 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180

Qy        197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 240

Qy        257 LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300

Qy        317 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDANRLWVDSKLVPFSGHM 360

Qy        377 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
              |||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db        361 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSTFVESQTYARENGQGDFAKCGFV 420

Qy        437 PSE 439
              |||
Db        421 PSE 423

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Job time : 163 secs
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```
PT   plant material and manure.
XX
PS   Claim 2; Page; 124pp; English.
XX
CC   The invention relates to novel active phytase variants (I) with one or
CC   more specific substitutions. The phytase variants of the invention are
CC   useful for improving the nutritional value of animal feed compositions
CC   (e.g. to increase growth rate, weight gain and/or feed conversion),
CC   reducing phytate levels in animal manure, treating vegetables or
CC   proteins, and liberating phosphorous from a phytase substrate. The
CC   present sequence represents a variant phytase of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ   Sequence 423 AA;

Query Match             96.5%;  Score 2244;  DB 7;  Length 423;
Best Local Similarity   99.5%;  Pred. No. 1.9e-216;
Matches   421;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP 60

Qy         77 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVVKFGVDDLLPFGANQSHQTGTDMYTRY 136
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVVKFGVDDLLPFGANQSHQTGTDMYTRY 120

Qy        137 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180

Qy        197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 240

Qy        257 LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300

Qy        317 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

Qy        377 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
              |||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db        361 TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSTFVESQTYARENGQGDFAKCGFV 420

Qy        437 PSE 439
              |||
Db        421 PSE 423

RESULT 15
ADI66843
ID   ADI66843 standard; protein; 423 AA.
XX
AC   ADI66843;
XX
DT   22-APR-2004  (first entry)
XX
DE   Peniophora lycii phytase mutant (1xviii).
XX
KW   phytase; nutritional value; growth rate; weight gain; feed conversion;
KW   mutant; mutein.
XX
OS   Peniophora lycii.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 334
FT                   /label= Wild-type A substituted by E
FT   Misc-difference 344
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OM protein - protein search, using sw model

Run on:      May 27, 2005, 08:27:23 ; Search time 171 Seconds
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Perfect score: 2325
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Total number of hits satisfying chosen parameters:      1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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               2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2325	100.0	439	2	Q96VH9	Q96vh9 peniophora
2	1204	51.8	442	2	Q96VK9	Q96vk9 cf. ceripor
3	1202	51.7	442	2	Q96VK8	Q96vk8 cf. ceripor
4	1160	49.9	443	2	Q96VF5	Q96vf5 trametes pu
5	1153	49.6	453	2	Q96VT0	Q96vt0 agrocybe pe
6	823	35.4	487	1	PHYA_THIHE	000107 thielavia h
7	776.5	33.4	467	2	Q9HEQ0	Q9heq0 aspergillus
8	773.5	33.3	596	2	Q7S9V5	Q7s9v5 neurospora
9	769	33.1	466	2	O00096	O00096 talaromyces
10	767.5	33.0	467	2	O93838	O93838 aspergillus
11	765.5	32.9	448	2	Q8J255	Q8j255 aspergillus
12	765.5	32.9	466	2	Q9C1T1	Q9c1t1 aspergillus
13	760.5	32.7	448	2	Q6GYA8	Q6gya8 aspergillus
14	760.5	32.7	448	2	Q6J336	Q6j336 aspergillus
15	759.5	32.7	467	1	PHYA_ASPNG	P34752 aspergillus
16	758.5	32.6	467	2	Q6T9Z6	Q6t9z6 aspergillus
17	754.5	32.5	467	1	PHYA_ASPAW	P34753 aspergillus
18	749.5	32.2	467	2	Q6R519	Q6r519 aspergillus
19	747.5	32.2	467	2	Q9UUZ7	Q9uuz7 aspergillus
20	744	32.0	466	2	O00100	O00100 aspergillus
21	742	31.9	465	1	PHYA_ASPFU	O00092 aspergillus
22	740	31.8	442	2	Q8WZJ5	Q8wzj5 aspergillus
23	738.5	31.8	463	1	PHYA_EMENI	O00093 emericella
24	724.5	31.2	466	1	PHYA_ASPTE	O00085 aspergillus
25	696.5	30.0	461	2	Q6YNE9	Q6yne9 penicillium
26	464	20.0	610	2	Q7SEH2	Q7seh2 neurospora
27	443.5	19.1	584	2	Q6CCS5	Q6ccs5 yarrowia li
28	412	17.7	463	1	PPA2_SCHPO	Q01682 schizosacch
29	397	17.1	482	2	Q8X1W7	Q8x1w7 monascus an
30	390.5	16.8	463	2	O60172	O60172 schizosacch
31	390	16.8	453	1	PPA1_SCHPO	P08091 schizosacch
32	388.5	16.7	464	2	Q6BUR8	Q6bur8 debaryomyce
33	385	16.6	468	1	PPA1_PICPA	P52291 pichia past
34	356	15.3	442	2	O74677	O74677 pichia angu
35	352	15.1	479	1	PHYB_ASPNG	P34754 aspergillus
36	348	15.0	479	1	PHYB_ASPAW	P34755 aspergillus
37	345.5	14.9	467	1	PPA5_YEAST	P00635 saccharomyc
38	342	14.7	461	2	Q6BM79	Q6bm79 debaryomyce
39	335.5	14.4	463	2	Q6BM75	Q6bm75 debaryomyce
40	335.5	14.4	467	1	PPA3_YEAST	P24031 saccharomyc
41	331.5	14.3	468	1	PPAD_YEAST	P52290 saccharomyc
42	315.5	13.6	467	1	PPAB_YEAST	P35842 saccharomyc
43	312.5	13.4	467	1	PPAC_YEAST	P38693 saccharomyc
44	301.5	13.0	469	2	Q6CYI2	Q6cyi2 kluyveromyc
45	298	12.8	484	2	Q6CLW3	Q6clw3 kluyveromyc

ALIGNMENTS

```
RESULT 1
Q96VH9
ID   Q96VH9        PRELIMINARY;      PRT;      439 AA.
AC   Q96VH9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase precursor (EC 3.1.3.26).
GN   Name=phyA;
OS   Peniophora lycii.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Lachnocladiaceae; Peniophora.
OX   NCBI_TaxID=154539;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21455028; PubMed=11571175;
RX   DOI=10.1128/AEM.67.10.4701-4707.2001;
RA   Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA   Wyss M., Fuglsang C.C.;
RT   "Expression, gene cloning and characterization of five novel phytases
RT   from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT   Ceriporia sp., and Trametes pubescens.";
RL   Appl. Environ. Microbiol. 67:4701-4707(2001).
DR   EMBL; AJ310696; CAC48195.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0008707; F:4-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR00056O; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW   Hydrolase; Signal.
FT   SIGNAL        1     29       Potential.
FT   CHAIN        30    439       Phytase.
SQ   SEQUENCE    439 AA;    47563 MW;  F668FA9DD3839DDA CRC64;
```

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Query Match             100.0%;   Score 2325;  DB 2;  Length 439;
Best Local Similarity   100.0%;   Pred. No. 7.3e-181;
Matches  439;  Conservative   0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy     61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVKFGVADLLPF 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVKFGVADLLPF 120

Qy    121 GANQSHQTGTGTDMYTRYSTLPEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GANQSHQTGTGTDMYTRYSTLPEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy    181 VVLQEEGNCTLCNMMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
```

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Db        ||||||||||||||||||||||||||||||
      181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy    241 CPFDTLSSGNASPFCDLFTAEEVYSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CPFDTLSSGNASPFCDLFTAEEVYSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy    301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy    361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy    421 YARNGQGDFAKCGFVPSE 439
          ||||||||||||||||||
Db    421 YARNGQGDFAKCGFVPSE 439
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```
RESULT 2
Q96VK9
ID   Q96VK9       PRELIMINARY;     PRT;    442 AA.
AC   Q96VK9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase precursor (EC 3.1.3.26).
GN   Name=phyA1;
OS   cf. Ceriporia sp. CBS 100231.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Ceriporia.
OX   NCBI_TaxID=154783;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 100231;
RA   Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA   Wyss M., Fuglsang C.C.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ310698; CAC48163.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0008707; F:4-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW   Hydrolase; Signal.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    442       Phytase.
SQ   SEQUENCE   442 AA;  47915 MW;  0464C1C691D86702 CRC64;

Query Match             51.8%;  Score 1204;  DB 2;  Length 442;
Best Local Similarity   55.3%;  Pred. No. 1.6e-89;
Matches  242; Conservative  51; Mismatches 139; Indels   6; Gaps    5;

Qy      1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
            |: |||||| |||| ||| | |: :|  ||  ||  |::| ||  | || ||| |||  ||
Db      1 MLFGFVALACLLSLLSSEVLATSVPKN-TAPTFPIPESEQRNWSPYSPYFPLAEYKAPPAGC 59
Qy     61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
            |::|||||:||||||||||||:|||||:||:||:: |:|||:|||||||:|:| ||||||
Db     60 QINQVNIIQRHGARFPTSGATTIKAGLTKLQGVQNFTDAKFNFIKSFKYDLGNSDLVPF 119
Qy    121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
            |||:|||:||::||||||||| :|:|||||||||||||||||||||||| :  |:|:|||
Db    120 GAAQSFDAGQEAFARYSKLVSKNNLPFIRADGSDRVVDSATNWTAGFASASHNTVQPKLN 179
Qy    181 VVLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMD 239
            :: :||||| :|||:||  | ||  ||||| |||  |||||||||| ||||| |||||:|
Db    180 LILPQTGNDTLEDNMCPAAGDSDPQVNAWLAVAFPSITARLNAAAPSVNLTDTDAFNLVS 239
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Qy    240 MCPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELL 297
            ||:|:|                :|| |||||||||||:|||||||||||| || ||||||
Db    240 LCAFLTVSKEKKSDFCTLFEGIPGSFEAFAYGGDLDKFYGTGYGQELGPVQGVGYVNELI 299
Qy    298 ARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPL 356
            |||  : ||::  ||||||  ||||||||| ||||||||||||||||| |: ::|  |||
Db    300 ARLTNSAVRDNTQTNRTLDASPVTFPLNKTFYADFSHDNLMVAVFSAMGLFRQPAPLSTS 359
Qy    357 KPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG--VDGVCELSAF 415
            ||  ||:| ||:|||||||||||:|  :|||| |:   |  | |::||    |  :||:
Db    360 VPNPWRTWRTSSLVPFSGRMVVERLSCFGTTKVRVLVQDQVQPLEFCCGDRNGLCTLAKF 419
Qy    416 VESQTYARENGQGDFAKC 433
            |||| |||.|||||| ||
Db    420 VESQTFARSDGAGDFEKC 437
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RESULT 3
Q96VK8
ID   Q96VK8       PRELIMINARY;     PRT;    442 AA.
AC   Q96VK8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase precursor (EC 3.1.3.26).
GN   Name=phyA2;
OS   cf. Ceriporia sp. CBS 100231.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Ceriporia.
OX   NCBI_TaxID=154783;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21455028; PubMed=11571175;
RX   DOI=10.1128/AEM.67.10.4701-4707.2001;
RA   Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA   Wyss M., Fuglsang C.C.;
RT   "Expression, gene cloning and characterization of five novel phytases
RT   from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT   Ceriporia sp.,and Trametes pubescens.";
RL   Appl. Environ. Microbiol. 67:4701-4707(2001).
DR   EMBL; AJ310699; CAC48164.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0008707; F:4-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW   Hydrolase; Signal.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    442       Phytase.
SQ   SEQUENCE   442 AA;  47552 MW;  483FAB442DB001EC CRC64;

Query Match             51.7%;  Score 1202;  DB 2;  Length 442;
Best Local Similarity   52.6%;  Pred. No. 2.4e-89;
Matches  230; Conservative  61; Mismatches 128; Indels  18; Gaps    5;

Qy      2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT 61
            : ||||||||||||||||||||||||||||||||||-------|||||||||||||||| |
Db     14 LSEVFAASVPRN-------------IAPKFSIPESEQRNWSPYSPYFPLAEYKAPPAGCE 60
Qy     62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
            :|||||||||||:|||||| :||||||||:||:|||||||:||||||||:|:|||||||
Db     61 INQVNIIQRHGARFPTSGAATRIKAGLSKLQSVQNFTDPKFDFPIKSFYTDLGTSDLVPFG 120
Qy    122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
            |||:|||:|||:||||| |||||||||||||:||||||:||||||||: :  :|:|: |
Db    121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNATQPKLDL 180
Qy    182 VLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
            |||||||| :|||:||  | ||  ||||| ||  :|||||||||| ||:||:|||||:|
Db    181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFFPSVIAQLNAAAPGNALTDADAFNLVSL 240
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Qy  241 CPPPTLSSGNASPPCDLFTA--EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVYVNELLA 298
        |||| |||||||| | ||  ::  :|||||||||||||||::||||||||||||  ||||||
Db  241 CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTGYGQALGPVQGVGYINELLA .300
Qy  299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
        ||| |||:|:|||||||||:|||||||:||||||||||||||||||||| ||| ||:|||
Db  301 RLTNSAVNDTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360
Qy  358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG--VDGVCELSAFV 416
        ||:||||| ||:||||||:||||| | |||||:|||||:||||:|:||  ||| ||:|| |
Db  361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRVLVQDQVQPLEFCGGDQDGLCALDKFV 420
Qy  417 ESQTYARENGQGDFAKC 433
        |||:||||:|||||:||
Db  421 ESQAYARSCGAGDFEKC 437
```

RESULT 4
Q96VF5
ID   Q96VF5   PRELIMINARY;   PRT;   443 AA.
AC   Q96VF5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase precursor (EC 3.1.3.26).
GN   Name=phyA;
OS   Trametes pubescens.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Aphyllophorales; Trametes.
OX   NCBI_TaxID=154538;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21455028; PubMed=11571175;
RX   DOI=10.1128/AEM.67.10.4701-4707.2001;
RA   Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA   Wyss M., Fuglsang C.C.;
RT   "Expression, gene cloning and characterization of five novel phytases
RT   from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT   Ceriporia sp. and Trametes pubescens.";
RL   Appl. Environ. Microbiol. 67:4701-4707(2001).
DR   EMBL; AJ310700; CAC48234.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0008707; F:4-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW   Hydrolase; Signal.
FT   SIGNAL   1   19   Potential.
FT   CHAIN   20   443   Phytase.
SQ   SEQUENCE   443 AA; 47773 MW; 13D4BEBCE0B049D1 CRC64;

Query Match   49.9%; Score 1160; DB 2; Length 443;
Best Local Similarity   52.0%; Pred. No. 6.3e-86;
Matches 230; Conservative 63; Mismatches 127; Indels 22; Gaps 7;

```
Qy    9 SILLSLMSSLALSTQFSFVAAQLPIPAQNTS----------NWGPYDFFPPVEPYAAPP 57
        |||| |: :  :: ||:|        :|:||          :||  |||| || | ||
Db    4 SILASL---LFVCYAYARAVPRAHIPLRDTSACLDVTRDVQQSWSMYSPYFPAATYVAPP 60
Qy   58 EGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADL 117
        | | ::|| :|||||||:|||||| |:| || ||::| |:|| : :   |: || ::| |
Db   61 ASCQINQVHIIQRHGARFPTSGAAKRIQTAVAKLKAASNYTDPLLAFVTNYTYSLGQDSL 120
Qy  118 LPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLP 177
        : ||| ||: | : :|||||:| : :|||||:|:| |||| : ||||||| |:|| || |
Db  121 VELGATQSSEAGQEAFTRYSSLVSADELPFVRASGSDRVVATANNWTAGFALASSNSITP 180
Qy  178 TLQVVLQEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALT 236
        || || |||||| |||||||||| | |||||||||||||||||||||||||| |:| ||
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Db  181 VLSVIISEAGNDTLDDNMCPAAGDSDPQVNQWLAQFAPPMTARLNAGAPGANLTDTFYN 240
Qy  237 LMDMCPFDTLSSGNASPFCDLF---TAEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVV 293
        | :|||| |||||||::|||    ::| || || |||||||||||||||||||||||||
Db  241 LLTLCPFETVATERRSEFCDIYEELQAED--AFAYNADLDKFYGTGYGQPLGPVQGVGYI 298
Qy  294 NELIARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA- 352
        ||||||||.|.|.||:|||.||||.||||||||||||||||||||| ||::||||:|:|
Db  299 NELIARLTAQNVSDHTQTNSTLDSSPETFPLNRTLYADFSHDNQMVAIFSAMGLFNQSAP 358
Qy  353 LDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG--VDGVCE 411
        |||  ||:||| || :|||||:||||||| | |:| |||||||:||||:|:||   || |
Db  359 LDPTTPDPARTFLVKKIVPFSARMVERLDCGGAQSVRLLVNDAVQPLAFCGADTSGVCT 418
Qy  412 LSAFVESQTYARENGQGDFAKC 433
        | |||||||:||:|| |||:|
Db  419 LDAFVESQAYARNDGEGDFEKC 440
```

RESULT 5
Q96VT0
ID   Q96VT0   PRELIMINARY;   PRT;   453 AA.
AC   Q96VT0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase precursor (EC 3.1.3.26).
GN   Name=phyA;
OS   Agrocybe pediades.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Bolbitiaceae; Agrocybe.
OX   NCBI_TaxID=84607;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21455028; PubMed=11571175;
RX   DOI=10.1128/AEM.67.10.4701-4707.2001;
RA   Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA   Wyss M., Fuglsang C.C.;
RT   "Expression, gene cloning and characterization of five novel phytases
RT   from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT   Ceriporia sp. and Trametes pubescens.";
RL   Appl. Environ. Microbiol. 67:4701-4707(2001).
DR   EMBL; AJ310697; CAC48160.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0008707; F:4-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW   Hydrolase; Signal.
FT   SIGNAL   1   19   Potential
FT   CHAIN   20   453   Phytase.
SQ   SEQUENCE   453 AA; 49931 MW; D62F1AEFA1091E5D CRC64;

Query Match   49.6%; Score 1153; DB 2; Length 453;
Best Local Similarity   51.3%; Pred. No. 2.4e-85;
Matches 232; Conservative 61; Mismatches 135; Indels 24; Gaps 7;

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Qy    4 SAFAPSILLSLMSSLALS--TQFSFVAAQLPIPAQNTSNWGPYDFFPVEVPEPYAAPEGCT 61
        | |   |:| |::::|.|  ||:|         :.|||:||  |||  : : | |   | |
Db    2 SLFIGGCLLVFLQASAYGGVVQATFV--QPFFPPQIQDSWAAYTPYPYPVQAYTPPPKDCK 59
Qy   62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
        :|||| |||||||:|||||  ||:|| ||::| |:||| |   |  || || : | ||||
Db   60 ITQVNIIQRHGARFPTSGAGTRIQAAVKKLQSAKTYTDPRLDFLTNYTYTLGHDDLVPFG 119
Qy  122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
        |.||.| : : :|||| |  ::| ||||:|..:|||| : || ||||   |  ||::| |
Db  120 ALQSSQAGEETFQRYSFLVSKENLPFVRASSNRVVDSATWTEGFSAASHVLNPILFV 179
Qy  182 VLQEGNCTLCNNMCPNEVDGDEST-TWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
        ||  ||||| |||||||||| | | ||||||||||||||||||||||||||| |:| |||
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```
Db    180  ILSESLNDTLDDAMCPNAGSSDPQTGIWTSIYGTPIANRLNQQAPGANITAADVSNLIPL  239
           :|  ||  ||   ||||       |||    ||     ||::::|| |
Qy    241  CPFDTLSSGNASPFCDLFTAEEVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL   300
           |:|:|                    :|:: |||:|||||||||||  ||:||:|||
Db    240  CAFETIVKETPSPFCNLFTPEEFAQFEYFGDLDKFYGTGYGQPLGPVQGVGYINELLARL  299

Qy    301  TGQAVRDETQTNRTLDSDPATPLNRTFYADFSHDNTMVPIFAALGLFN-ATALDPLKPD  359
           ||| |  |||||||||||:  ||||:|||||||||||||  |:||  ||  | |:|
Db    300  TEMPVRDNTQTNRTLDSSPLTFPLDRSIYADLSHDNQMIAIFSAMGLFNQSSPLDPSFPN  359

Qy    360  ENRLWVDSKLVPFSGHMTVEKLAC------SG------KEAVRVLVNDAVQPLEF  402
           ||:||: |:| ||||||||||:|        |         ||:|:||:|||:|
Db    360  PKRTWVTSRLTPFSARMVTERLLCQRDGTGSGGPSRIMRNGNVQTFVRILVNDALQPLKF  419

Qy    403  CGG-VDGVCELSAFVESQTYARENGQGDFAKC  433
           ||| ||| ||||||:|||||||||||||| |
Db    420  CGGDMDSLCTLEAFVESQKYAREDGQGDFEKC  451


RESULT 6
PHYA_THIHE
ID    PHYA_THIHE    STANDARD;      PRT;     487 AA.
AC    O00107;
DT    29-MAR-2004  (Rel. 43, Created)
DT    29-MAR-2004  (Rel. 43, Last sequence update)
DT    05-JUL-2004  (Rel. 44, Last annotation update)
DE    3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-
DE    phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate
DE    phosphohydrolase A).
GN    Name=PHYA;
OS    Thielavia heterothallica (Myceliophthora thermophila).
OC    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC    Sordariomycetidae; Sordariales; Chaetomiaceae; Corynascus.
OX    NCBI_TaxID=78579;
RN    [1]
RP    SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX    MEDLINE=97177792; PubMed=9025298;
RA    Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L.,
RA    van Loon A.P.G.M.;
RT    "The phytase subfamily of histidine acid phosphatases: isolation of
RT    genes for two novel phytases from the fungi Aspergillus terreus and
RT    Myceliophthora thermophila.";
RL    Microbiology 143:245-252(1997).
CC    -!- FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
CC        from phytate.
CC    -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
CC        myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC    -!- SUBCELLULAR LOCATION: Secreted.
CC    -!- MISCELLANEOUS: Shows activity with phytic acid at a pH range of
CC        3.5 to 8.5, with maximal activity between pH 5.5 and 6.0. Also
CC        accept 4-nitrophenyl phosphate as substrate with a pH optima
CC        shifted to more acidic pH values.
CC    -!- SIMILARITY: Belongs to the histidine acid phosphatase family.
CC    --------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; U59806; AAB52508.1; -.
DR    HSSP; P34752; 1IHP.
DR    InterPro; IPR000560; HisAc_phsphtse.
DR    Pfam; PF00328; Acid_phosphat_A; 1.
DR    PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR    PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW    Glycoprotein; Hydrolase; Signal.
FT    SIGNAL         1     19       Potential.
FT    CHAIN         20    487       3-phytase A.
FT    DOMAIN       423    433       Poly-Gly.
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FT    ACT_SITE       75     75              Nucleophile (By similarity).
FT    ACT_SITE      369    369              Proton donor (By similarity).
FT    DISULFID       26     35              By similarity.
FT    DISULFID       64    421              By similarity.
FT    DISULFID      208    485              By similarity.
FT    DISULFID      260    289              By similarity.
FT    DISULFID      456    464              By similarity.
FT    CARBOHYD      165    165              N-linked (GlcNAc...) (Potential).
FT    CARBOHYD      200    200              N-linked (GlcNAc...) (Potential).
FT    CARBOHYD      247    247              N-linked (GlcNAc...) (Potential).
FT    CARBOHYD      346    346              N-linked (GlcNAc...) (Potential).
SQ    SEQUENCE   487 AA;  52537 MW;  97D10EDC83D051DB CRC64;

Query Match             35.4%;  Score 823;  DB 1;  Length 487;
Best Local Similarity   43.2%;  Pred. No. 2.1e-58;
Matches 192;  Conservative 52;  Mismatches 142;  Indels 58;  Gaps 13;

Qy     41  WGPYDPFF--PVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFT   98
           ||:| ||                 :|| | :|  :|::|            ::
Db     43  WGQYSPYFSVPSELDASIPDDCEVTFAQVLSRHGARAPTLKRAASYVDLDRIHHGAISY  102

Qy     99  DPKYEFLNDFVYKPGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVD  158
           | || |  |           || ||  |  |  :|| || |        ||
Db    103  GPGYEFLRTYDYTLGADELTRTGQQOMVNSGIKFYRYRYRALAR-KSIPFYRTAGQDRVVH  161

Qy    159  SSTNWTAGFGDA----SGETVLPTL---QVVLQBE--GNCTLCNNMC---------PNEVDGD  203
           ::|: | ||                : |:  ::   |
Db    162  SAENFTQGFHSALLADRGSTVRPTLPYDMVVIPETAGANNTLHNDLCTAFEEGPYSTIGD  221

Qy    204  ES-TTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSS--------------GN  250
           ::  :               || |        ::   :::
Db    222  DAQDTYLSTFAGPITARVNANLPGANLTDADTVALMDLCPFETVASSSSDPATADAGGGN  281

Qy    251  A---SPFCDLFTAEEVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRD  307
           |       |:| ||||| :: |||||||||:||||:||:||:|||:|||:|||||:
Db    282  GRPLSPFCRLFSESEWRAYDYLQSVGKWYGYGPGNPLGPTQGVGFVNELLARLAGVPVRD  341

Qy    308  ETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPL------KPDEN  361
           ||:|||||| | || :|| ||||||||||| ||||||| ||  ||
Db    342  GTSTNRTLDGDPRTFPLGRPLYADFSHDNDMGVLGALGAYD--GVPPLDKTARRDPEEL  399

Qy    362  RLWVDSKLVPFSGHMTVEKLACSG--------------KEAVRVLVNDAVQPLEFCGGV  406
           :              :|||| ||              |||:|:||:| |||||||||
Db    400  GGYAASWAVPFAARIYVEKMRCSGGGGGGGGGEGRQEKDEEMVRVLVNDRVMTLKGCGAD  459

Qy    407  D-GVCELSAFVESQTYARENGQGD  429
           : |  ||||||||||||||:|:||
Db    460  ERGMCTLERFIESMAFARGNGKWD  483


RESULT 7
Q9HEQ0
ID    Q9HEQ0         PRELIMINARY;    PRT;     467 AA.
AC    Q9HEQ0;
DT    01-MAR-2001  (TrEMBLrel. 16, Created)
DT    01-MAR-2001  (TrEMBLrel. 16, Last sequence update)
DT    01-MAR-2004  (TrEMBLrel. 26, Last annotation update)
DE    Phytase.
OS    Aspergillus ficuum.
OC    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC    Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX    NCBI_TaxID=5058;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Zhang L., An L., Wang Y., Yuan X.;
RL    Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AY013315; AAG40885.1; -.
DR    HSSP; P34752; 1IHP.
DR    GO; GO:0003993; F:acid phosphatase activity; IEA.
DR    InterPro; IPR000560; HisAc_phsphtse.
DR    Pfam; PF00328; Acid_phosphat_A; 1.
DR    PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR    PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
```

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SQ   SEQUENCE   467 AA;   51012 MW;   3F69AD543C0B565B CRC64;

Query Match
Best Local Similarity   33.4%;   DB 2;   Length 467;
                        38.4%;   Pred. No. 1.2e-54;
Matches 188;  Conservative 62;  Mismatches 156;  Indels 83;  Gaps 17;

Qy    2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPA----QNTSN------------------WGP 43
          ||||:::  | |||||||||||:::         |:
Db    3 VSAVLLPLYLL----------SGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQ 50

Qy   44 YDPFFPVEPYAA---PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD 99
Db   51 YAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFE 110

Qy  100 PKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMTRYSTLFEGGDVPFVRAAGDQRVVDS 159
Db  111 GKYAPLKTYNYSLGADDLLTPFGEQELVNSGVKFYQRYESLTR-NIVPFIRSSGGSRVIAS 169

Qy  160 STNWTAGF------------------GDASGETVLPTLQVVLQE------------EGNCTLCNNMCPN 198
Db  170 GNKFIEGFQSTKLKDPRAQPGQSS-----PKIDVVISEASTSNNTLDPGTCTVFED---S 221

Qy  199 EVDGDESTTWLGVFAPNITARLNAAAPASANLSDSDALTLMDMCPFDTLSSGNA----SPF 254
Db  222 ELADDIEANFTATFVPSIRQRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPF 281

Qy  255 CDLFTAEEVSVSYEYYYDLDKYYGTGPGNALGPVQVGVGYVNELLARLTGQAVRDETQTNRT 314
Db  282 CDLFTHEEWINYDYLQSLNKYYGHGAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHT 341

Qy  315 LDSDDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD-----SK 368
Db  342 LDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSSTTAENITQTDGFSSAR 399

Qy  369 LVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTYARE 424
Db  400 TVPFASRMTVEMMQCQSEQEPLVRVLVNDRVVPLHGC--PVDALGRCTRDSFVKGLSFARS 458

Qy  425 NGQGDFAKC 433
          ||:|
Db  459 G--GDWAEC 465
```

RESULT 8
Q7S9V5

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ID   Q7S9V5        PRELIMINARY;      PRT;   596 AA.
AC   Q7S9V5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=NCU06351.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann H., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000209; EAA33149.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   596 AA;   65281 MW;   7085B991224AE410 CRC64;

Query Match
Best Local Similarity   33.3%;   DB 2;   Length 596;
                        37.6%;   Pred. No. 2.9e-54;
Matches 195;  Conservative 65;  Mismatches 158;  Indels 101;  Gaps 19;

Qy   10 ILLLSMSSLALSTQFSFVAAQ----------LPIPA---------QNTSNWGPYDPFFPVE 51
Db   82 IFVKLIMFLLMVPLFSYLAAASLRVLSPNPASCDSPELGYQCNSETTHTWGQYSPFFSVP 141

Qy   52 PYAAP--PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFV 109
Db  142 SEISPSVPEGCRLTFAQVLSRHGARPPTPGKAAAISAVLTKIKTSATWYAPDFBFIKDYN 201

Qy  110 YKFGVADLLPFGANQSHQTGTDMTRYSTLF-----EGGDVPFVRAAGDQRVVDSSTNWTA 165
Db  202 YVLGVDHLTAFGEQEMVNSGIKFYQRYASLIRDYTDPESLPFIRASGQERVIASAENFTT 261

Qy  166 GFGDA----------SGETVLPTLQVVLQEE---GNCTLCNNMC----PNEVDGDES-TTWLG 210
Db  262 GFYSALLADKNPPPSSLPLPRQEMVIISESPTANNTMHGLCRAFEDSTTGDAAQATFIA 321

Qy  211 VFAPNITARLNAAA-PSANLSDSDALTLMDMCPFDTLS----------SGNA--SPF 254
Db  322 ANFPPITARLNAQGFKGVTLSDTDVLSLMDLCPFDTVAYPPSSSLITSSSPSGGSKLSPF 381

Qy  255 CDLFTAEEVSYEYYYDLDKYYGTGPGNALGPVQVGVGYVNELLARLTGQAVRDETQTNRT 314
Db  382 CSLFTAQDFTVYDYLQSLGKFYGYGPGNSLAATQGVGYVNELLARLTVSPVVDNTTTTNST 441

Qy  315 LDSDDPATFPL--NRTFYADFSHDNTMVPIFAALGLFNA------------TALD 354
Db  442 LDGNEDTFPLSRNRTVFADFSHDNDMMGIILTALRIFEGVDAEKMDNTTIPREYGETGDD 501

Qy  355 P--LKPDENRL---WVDSKLVPFSGHMTVEKLACSG----------KEAVRVLVND 395
Db  502 PANLKEREGLFKVGWV-----VPFRARVYFEKMICDGDGSGEMVQSEEEQDKELVRILVND 557

Qy  396 AVQPLEFCGGVD-GVCELSAFVESQTYARENGQGDFAKC 433
Db  558 RVVKLNGCEADELGRCKLDKFVESMEFARRG--GDWDKC 594
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RESULT 9
Q00096

```
ID   Q00096        PRELIMINARY;      PRT;   466 AA.
AC   Q00096;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase (EC 3.1.3.8).
OS   Talaromyces thermophilus.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Talaromyces.
OX   NCBI_TaxID=28565;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98007872; PubMed=9349716; DOI=10.1016/S0167-4781(97)00107-3;
RA   Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
RA   van Loon A.P.;
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RT   "Cloning of the phytases from Emericella nidulans and the thermophilic
RT   fungus Talaromyces thermophilus.";
RL   Biochim. Biophys. Acta 1353:217-223(1997).
DR   EMBL; U59802; AAB96873.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0016158; F:3-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW   Hydrolase.
SQ   SEQUENCE   466 AA;   51450 MW;   FC457B521A5C929 CRC64;

Query Match   33.1%; Score 769; DB 2; Length 466;
Best Local Similarity   42.8%; Pred. No. 4.9e-54;
Matches 184; Conservative 49; Mismatches 149; Indels 48; Gaps 16;

Qy   40 NWGFYDPFPV--EPYAAP--PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMAR 95
              | |||| : |||||| || : || :||
Db   44 SWGQYSPFFSLADQSEISPDVPQNCKITFVQLLSRHGARYPTSSKTELYSQLISRIQKTA 103

Qy   96 PFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQR 155
              || |||||||||||| ||||||||||||||| |||
Db   104 TAYKGYYAPLKDYRYQLGANDLTPFGENQMIQLGIKFYNHYKSLARNA-VPFVRCSGSDR 162

Qy   156 VVDSSTNWTAGFGDASGETVL-----------PTLQVVLQEEG--NCTLCNNMCPNEVDG 202
              |: :|| || || ||| ||:
Db   163 VIASGRLFIEGFQSAK---VLDPHSDKHDAPPTINVII-EEGPSYNNTLDTGSCPVFEDS 218

Qy   203 ----DESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA---SPFC 255
                  |||||||| |||||||||| |||||| ||||| ||||||||||||||
Db   219 SGGHDAQEKFAKQFAPAILEKIKDHLPGVDLAVSDVPYIMDLCPFETLARNHTDTLSPFC 278

Qy   256 DLFTABEVSYEYYYDLDKYYGTGPGNALGPVQVGVYNELLARLTGQAVRDETQTNRTL 315
              |||||||||||||||||||||||||||||||||| ||| |||||||
Db   279 ALSTQEEWQAYDYTYQSLGKYYGNGQGGNPLGPAQGVGFVNELIARMTHSPVQDYTTVNHTL 338

Qy   316 DSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA------LDPLKPDE----NRLWVDS 367
              |||||||||||||||||||||||||||||||||| ||
Db   339 DSNPATFPLNATLYADFSHDNTMTSIFAALGLYNGTAKLSTTEIKSIRETDGYSAAWT-- 396

Qy   368 KLVPFSGHMTVEKLAC--SGKEAVRVLVNDAVQPLEFCCGVD--GVCELSAFVESQTYAR 423
              ||||||||||||||| |: ||||||||||| ||| | | || | |||||| | |
Db   397 --VPFGGRAYIEMMQCDDSDEPVVRVLVNDRVVPLHGC-EVDSLGRCKRDDFVRGLSFAR 453

Qy   424 ENG--QGDFPA 431
              :||:|::|
Db   454 QGGNWEGCYA 463

RESULT 10
O93838
ID   O93838;   PRELIMINARY;   PRT;   467 AA.
AC   O93838;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase.
GN   Name=phyA;
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SK-57;
RA   Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB022700; BAA74433.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.

DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ   SEQUENCE   467 AA;   51028 MW;   7A38AD543EDC265C CRC64;

Query Match   33.0%; Score 767.5; DB 2; Length 467;
Best Local Similarity   38.2%; Pred. No. 6.5e-54;
Matches 187; Conservative 61; Mismatches 158; Indels 83; Gaps 17;

Qy   2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPA---QNTSN---------WGP 43
              | | :
Db   3 VSAVLLPLYIL----------SGVTSGLAVPASRNQSTCDTVDGYQCFSETSHLWGQ 50

Qy   44 YDPFFPVEPYAA---PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD 99
              |:|| || || : |:||||||||| ||| :||:|
Db   51 YAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFE 110

Qy   100 PKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDS 159
              | |||||||| ||||||||||||||||||||||||||| : || |
Db   111 GKYAFLKTYNYSLGADDLTPFGEQLVNSGVKFYQRYESLTR-NIVPFIRSSGSSRVIAS 169

Qy   160 STNWTAGF----------GDASGETVLPTLQVVLQE-----EGNCTLCNNMCPN 198
              :: || | ||:
Db   170 GNKFIEGFQSTKLKDPRAQPGQSS----PKIDVVISEASTSNNTLDPGTCTVFED---S 221

Qy   199 EVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----SPF 254
              ||| |||||||| ||||||| ||| ||||||| ||| ||||||||||||||
Db   222 ELADDIEANFTATFVPSIRQRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPF 281

Qy   255 CDLFTABEVSYEYYYDLDKYYGTGPGNALGPVQVGVYNELLARLTGQAVRDETQTNRT 314
              ||||| |||||||||||||||||| || |||| | ||| ||| |||
Db   282 CDLFTHEEWINYDYLQSLNKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHT 341

Qy   315 LDSDPATPPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD----SK 368
              |||||| | ||||||||||||||| |||||:|||| | | : : ||||
Db   342 LDSNPATFPLNSTLYADFSHDNGIISILPALGLYNGT--KPLSSTTAENITQTDGFSSAW 399

Qy   369 LVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCCGVD--GVCELSAFVESQTYARE 424
              ||||||||||||| :||||||||||| ||| | || | ||||| ||
Db   400 TVPFASRMVEMMQCQSEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVKGLSFARS 458

Qy   425 NGQGDFAKC 433
              :|:|::
Db   459 G--GDWGEC 465

RESULT 11
Q8J255
ID   Q8J255;   PRELIMINARY;   PRT;   448 AA.
AC   Q8J255;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase (Fragment).
GN   Name=phyA;
OS   Aspergillus ficuum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5058;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Li G., Zhu J., Sun J., Wu Z., Wang L., Chen G., Jiang H., Li M.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF53744; AAN10115.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   448 AA;   49260 MW;   0554FF9712FF7BAA CRC64;

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Query Match          32.9%;
Best Local Similarity  40.7%;   Score 765.5;   DB 2;   Pred. No. 8.9e-54;
Matches  176;   Conservative  55;   Mismatches 148;   Indels  53;   Gaps  14;

Qy   41  WGPYDPFFPVEPYAA---PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP   96
         ||  | |  | :|:|      :: | |||||||||||| ::  |  :|| ::|
Db   29  WGQYAPFFSLANKSAISPDVPAGCQVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT  88

Qy   97  FTDPKYEFLNDFVVKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV  156
         || ||| | :| ||||||||||||| |  ||||||||||| ||  ||| :
Db   89  TFEEKYAFLKTYNYSLGADDLTPFGEQELVNSGVKFYQRYESLTR-NIVPFIRSSGSSRV 147

Qy  157  VDSSTNWTAGF---------GDASGETVLPTLQVVLQE------EGNCTLCNNM       195
         :||  |   | :         |||:|   | |||||||      | | | ||
Db  148  IASGNKFIEGFQSTKLKDPRAQPGQSS-----PKIDVVISEASTSNNTLDPGTCTVFED- 201

Qy  196  CPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA---- 251
            :|| |  :  : |  | :   | |:|||| | |||||||||| ||||| |:
Db  202  --SELADDIEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKL 259

Qy  252  SPFCDLFTAEBYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQT 311
         |||||||  |  : |:| | :|||| | ||||| |||||||||||:||| |
Db  260  SPFCDLFTHEEWINYDYLQSLNKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSS 319

Qy  312  NRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD--- 366
         | ||||:||||||| | |||||||| : :|:|||||:| |    | |    || | :
Db  320  NHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSSTTAENITQTDGFS 377

Qy  367  -SKLVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTY 421
          : :|||:  : ||::| |::| :||||||||:|:||: | ||   || | ||||:|:|
Db  378  SAWTVPFASRMYVEMMQCCQSEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVKGLSF 436

Qy  422  ARENGQGDFAKC 433
         || || || ||
Db  437  ARSG--GDWAEC 446


RESULT 12
Q9C1T1
ID   Q9C1T1        PRELIMINARY;      PRT;    466 AA.
AC   Q9C1T1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phytase.
GN   Name=phyA;
OS   Aspergillus oryzae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5062;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gomi K.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB042805; BAB40715.1; -.
DR   HSSP; P34752; 1IHP.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
SQ   SEQUENCE   466 AA;  51257 MW;  8033BED57FBA2791 CRC64;

Query Match          32.9%;
Best Local Similarity  38.1%;   Score 765.5;   DB 2;   Pred. No. 9.4e-54;
Matches  179;   Conservative  65;   Mismatches 171;   Indels  55;   Gaps  16;

Qy    9  SILLSLMSSLALSTQFSFVAAQLPIPAQNTSN-----------------WGPYDPFFPVEPY  53
         |:|   :   |:   |::           |                   |||||||||||
Db    5  SVLLPITFLLS-----SVTGTPVTSPRQQSCNTVDEGYQCFSGVSHLMGQYSPYFSVDDE  59

Qy   54  AA---PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARFPTDPKYEFLNDFV  109
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Db   60  SSLSEDVPDHCQVTFAQVLSRHGARYPTKSKSEKYAKLIKAVQHNATSFSGKYAFLKSYN 119
         : :| :  | ||||||||:|||||: |:|:|::|||::|| ||:||:|:|||| ||: |
Qy  110  YKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGF-- 167
         : | |||:|||| |  :||||||||||||||||||:||:|||| || |:|  |  |
Qy  120  YSLGADDLITPFGENQLVDSGIKFYQRYEELAK-NVVPFIRASGSDRVIASGEKFIEGFQK 178

Qy  168  ---GDASGE--TVLPTLQVVLQE-EG-NCTLCNMC---PNEVDGDES-TTWLGVFAPNI  216
            ||:||   | | ||||||||  | ||||| |     |||||| || | |  ||| :
Qy  179  AKLGDSKSKRGQPAPIVNVVITETEGFNNTLDHSLCTAFENSTTGDDAEDKFTAVFTPSI 238

Qy  217  TARLNAAAPSANLSDSDALTLMDMCPFDTLS----SGNASPFCDLFTAEBYVSYEYYYDL 272
          :||:| ||| | |||||| |||||:|||:     ||:||||||||| |  : |:| | :
Db  239  VERLEKDLPGTTLSSKEVVYLMDMCSFDTIALTRDGSRLSPFCALFTQEEWAQYDYLQSV 298

Db  273  DKYYGTGPNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADF  332
         :|||| | ||||||||||||||:|||| |   : |  | ||||:||||||| | |||
Qy  299  SKYYGYGGGNPLGPAQGIGFANELIARLITKSPVKDHTTTNTTLDSNPATFPLNATLYADF 358

Qy  333  SHDNTMVPIFAALGLFNATALDPL-------KPDENRLWVDSKLVPFSGHMTVEKLACSGK 386
         |||||: :|: |||||:|  | ||        : | : :|  |:||||| |||  |
Db  359  SHDNTMTSVFFALGLYNTT--EPLSQTSVQSTEETNGYSSARTVPFGARAYVEMQCTDE  416

Qy  387  E--AVRVLVNDAVQPLEFCCGVD-GVCELSAFVESQTYARENGQCDFAKC 433
             |||||||||:|:|| |  |   || | |||:|| | |: | | | |
Db  417  KEPLVRVLVNDRVIPLQGCDADEYGRCKRDDFVEGLSFVTSG--GNWGEC 464


RESULT 13
Q6GYA8
ID   Q6GYA8        PRELIMINARY;      PRT;    448 AA.
AC   Q6GYA8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Phytase (EC 3.1.3.8) (Fragment).
GN   Name=phyA;
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N-2;
RA   Wu J., Yan C.Y.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY615712; AAT51735.1; -.
DR   GO; GO:0016158; F:3-phytase activity; IEA.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW   Hydrolase.
FT   NON_TER      1      1
SQ   SEQUENCE   448 AA;  49170 MW;  C319E1FECEB4EF18 CRC64;

Query Match          32.7%;
Best Local Similarity  40.5%;   Score 760.5;   DB 2;   Pred. No. 2.3e-53;
Matches  175;   Conservative  56;   Mismatches 148;   Indels  53;   Gaps  14;

Qy   41  WGPYDPFFPVEPYAA---PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP   96
         ||  | |  | :|:|      :: | |||||||||||| ::  |  :|| ::|
Db   29  WGQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT  88

Qy   97  FTDPKYEFLNDFVVKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV  156
         || ||| | :| ||||||||||||| |  ||||||||||| ||  ||| :
Qy   89  TFEGKYAFLKTYDYSLGADDLTPFGEQELVNSGVKFYQRYESLTR-NIVPFIRSSGSSRV 147

Qy  157  VDSSTNWTAGF---------GDASGETVLPTLQVVLQE------EGNCTLCNNM       195
         :||  |   | :         |||:|   | |||||||      | | | ||
Db  148  IASGNKFIEGFQSTKLKDPRAQPQSS-----PKIDVVISEASTSNNTLDPGTCTVFED- 201
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Db   320 NHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSSTTAENITQTDGFS 377

Qy   367 -SKLVPFSGHMTVEKLACSGKE-AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTY 421

Db   378 SAWTVPFASRMYVEMMQCQSEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVKGLSF 436

Qy   422 ARENGQGDFAKC 433

Db   437 ARSG--GDWGEC 446


RESULT 15
PHYA_ASPNG
ID   PHYA_ASPNG     STANDARD;      PRT;    467 AA.
AC   P34752;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-
DE   phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate
DE   phosphohydrolase A).
GN   Name=PHYA;
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
RX   MEDLINE=93252284; PubMed=8387447; DOI=10.1016/0378-1119(93)90620-I;
RA   van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M., Gouka R.J.,
RA   Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A., Selten G.C.M.,
RA   Veenstra A.E., van Gorcom R.F.M., van den Hondel C.A.M.J.J.;
RT   "Cloning, characterization and overexpression of the phytase-encoding
RT   gene (phyA) of Aspergillus niger.";
RL   Gene 127:87-94(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Mullaney E.J.;
RT   "Sequence of the Aspergillus niger (ficuum) phytase gene.";
RL   Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 24-464.
RC   STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
RX   MEDLINE=93249451; PubMed=8387289;
RA   Ullah A.H.J., Dischinger H.C. Jr.;
RT   "Aspergillus ficuum phytase: complete primary structure elucidation by
RT   chemical sequencing.";
RL   Biochem. Biophys. Res. Commun. 192:747-753(1993).
RN   [4]
RP   SEQUENCE OF 71-93.
RC   STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
RX   MEDLINE=91298982; PubMed=1648914;
RA   Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.;
RT   "Cyclohexanedione modification of arginine at the active site of
RT   Aspergillus ficuum phytase.";
RL   Biochem. Biophys. Res. Commun. 178:45-53 (1991).
RN   [5]
RP   CHARACTERIZATION, AND PARTIAL SEQUENCE.
RC   STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
RX   MEDLINE=89160685; PubMed=2852807;
RA   Ullah A.H.J.;
RT   "Aspergillus ficuum phytase: partial primary structure, substrate
RT   selectivity, and kinetic characterization.";
RL   Prep. Biochem. 18:459-471(1988).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC   STRAIN=NRRL 3135 / Van Tieghem / Ficuum;
RX   MEDLINE=97307250; PubMed=9164457;
RA   Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D.,
RA   van Loon A.P.G.M.;
RT   "Crystal structure of phytase from Aspergillus ficum at 2.5-A
RT   resolution.";
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Qy   196 CPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA---- 251

Db   202 --SELADDIEANFTATFVPSIRQRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKL 259

Qy   252 SPFCDLFTAEEVVSYEYYYDLDKYYGTGPGNALGPVQGVGYANELLARLTGQAVRDETQT 311

Db   260 SPFCDLFTHEEWINYDYLQSLNKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSS 319

Qy   312 NRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD--- 366

Db   320 NHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSSTTAENITQTDGFS 377

Qy   367 -SKLVPFSGHMTVEKLACSGKE-AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTY 421

Db   378 SAWTVPFASRMYVEMMQCQSEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVKGLSF 436

Qy   422 ARENGQGDFAKC 433

Db   437 ARSG--GDWGEC 446


RESULT 14
Q6J336
ID   Q6J336     PRELIMINARY;      PRT;    448 AA.
AC   Q6J336;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Phytase (Fragment).
OS   Aspergillus oryzae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5062;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nong Y., He Y., Rachid L., Wu Z., Qing Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY603416; AAT12504.1; -.
DR   GO; GO:0003993; F:acid phosphatase activity; IEA.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   448 AA;  49169 MW;  FBABFCDE20140514 CRC64;

Query Match              32.7%;  Score 760.5;  DB 2;  Length 448;
Best Local Similarity    40.5%;  Pred. No. 2.3e-53;
Matches  175;  Conservative  56;  Mismatches  148;  Indels  53;  Gaps  14;

Qy    41 WGPYDPFFVEPYAA---PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP 96

Db    29 WGGYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT 88

Qy    97 FTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV 156

Db    89 TPEGKYAFLKTYNYSLGADDLTPFGEQELVNSGVKFYQRYESLTR-NIVPFIRSSGSSRV 147

Qy   157 VDSSTNWTAGF----------GDASGETVLPTLQVVLQE---------EGNCTLCNNM 195

Db   148 IASGNKFIEGFQSTKLKDPRAQPGQSS-----PKIDVVISEASTSNNTLDPGTCTVFED- 201

Qy   196 CPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA---- 251

Db   202 --SELADDIEANFTATFVPSIRQRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKL 259

Qy   252 SPFCDLFTAEEVVSYEYYYDLDKYYGTGPGNALGPVQGVGYANELLARLTGQAVRDETQT 311

Db   260 SPFCDLFTHEEWINYDYLQSLNKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSS 319

Qy   312 NRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD--- 366
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RL   Nat. Struct. Biol. 4:185-190(1997).
CC   -!- FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
CC       from phytate.
CC   -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
CC       myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- BIOTECHNOLOGY: Is used as a food and feed additive. It can
CC       facilitate the degradation of phytin in soybean and other seeds
CC       used as food for monogastric animals. Sold by Novo Nordisk under
CC       the name Phytase Novo.
CC   -!- SIMILARITY: Belongs to the histidine acid phosphatase family.
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DR   EMBL; Z16414; CAA78904.1; -.
DR   EMBL; M94550; AAA32705.1; -.
DR   PIR; JN0482; JN0482.
DR   PIR; JN0656; JN0656.
DR   PDB; 1IHP; X-ray; @=30-467.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; Acid_phosphat_A; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW   3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
KW   Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    467       3-phytase A.
FT   ACT_SITE     82     82       Nucleophile (By similarity).
FT   ACT_SITE    362    362       Proton donor (By similarity).
FT   DISULFID     31     40
FT   DISULFID     71    414
FT   DISULFID    215    465
FT   DISULFID    264    282
FT   DISULFID    436    444
FT   CARBOHYD     27     27       N-linked (GlcNAc...).
FT   CARBOHYD     59     59       N-linked (GlcNAc...).
FT   CARBOHYD    105    105       N-linked (GlcNAc...).
FT   CARBOHYD    120    120       N-linked (GlcNAc...).
FT   CARBOHYD    207    207       N-linked (GlcNAc...).
FT   CARBOHYD    230    230       N-linked (GlcNAc...).
FT   CARBOHYD    339    339       N-linked (GlcNAc...).
FT   CARBOHYD    352    352       N-linked (GlcNAc...).
FT   CARBOHYD    376    376       N-linked (GlcNAc...).
FT   CARBOHYD    388    388       N-linked (GlcNAc...).
FT   STRAND       32     33
FT   TURN         34     36
FT   STRAND       37     38
FT   TURN         40     41
FT   HELIX        42     45
FT   TURN         46     47
FT   HELIX        49     51
FT   STRAND       53     53
FT   HELIX        55     55
FT   TURN         58     60
FT   HELIX        69     70
FT   STRAND       71     81
FT   STRAND       85     85
FT   HELIX        89    105
FT   HELIX       111    118
FT   STRAND      128    128
FT   HELIX       130    146
FT   TURN        147    147
FT   HELIX       148    151
FT   TURN        152    153
FT   STRAND      157    161
FT   HELIX       164    182
FT   TURN        183    183
FT   TURN        185    186
FT   TURN        189    190
FT   STRAND      196    200
FT   TURN        204    205
FT   TURN        209    210
FT   HELIX       216    220
FT   HELIX       223    233
FT   TURN        234    235
FT   HELIX       236    246
FT   TURN        248    249
FT   HELIX       254    269
FT   TURN        270    284
FT   HELIX       280    305
FT   HELIX       287    308
FT   HELIX       305    312
FT   TURN        307    316
FT   TURN        310    328
FT   HELIX       313    343
FT   TURN        317    348
FT   HELIX       329    360
FT   TURN        340    371
FT   HELIX       346    377
FT   TURN        355    394
FT   STRAND      362    400
FT   HELIX       372    403
FT   TURN        389    404
FT   HELIX       397    414
FT   STRAND      403    426
FT   TURN        404    428
FT   STRAND      404    430
FT   STRAND      406    441
FT   TURN        421    445
FT   STRAND      427    452
FT   TURN        429    457
FT   STRAND      440    461
FT   HELIX       444    465
FT   HELIX       446    467
FT   HELIX       454
FT   HELIX       458
FT   TURN        462
FT   TURN        466
SQ   SEQUENCE   467 AA;  51086 MW;  88FE8F358434lD6D CRC64;
```

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Query Match              32.7%;          Score 759.5;   DB 1;   Length 467;
Best Local Similarity    38.2%;          Pred. No. 2.9e-53;
Matches 187;   Conservative 58;   Mismatches 161;   Indels 83;   Gaps 18;

Qy    2  VSSAFAPSILLSLMSSLALSTQPSFVAAQLPIPA-QNTSN------------------WGP   43
         |||   : |||:| :::| ||  :                                  ||
Db    3  VSAVLLPLYLL---------SGVTSGLAVPASRNQSSCDTVDGQYQCFSETSHLWGQ        50

Qy   44  YDPFFPV--EPYAAP--PEGCTVIQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD   99
         | ||  :     :    || :|| ||  |||||:||   || ::  :    ||::: |||
Db   51  YAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKKYSALIEEIQQNATTFD  110

Qy  100  PKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDS  159
         .||.||   |  ||.|||.|||.|   :| ||||: |: || . || ||::|: ||: :
Db  111  GKYAFLKTYNYSLGADDLTPFGEQEIVNSGIKFYQRYESLTR-NIVPFIRSSGSSRVIAS  169

Qy  160  STNWTAGF--------------GDASGETVLPTLQVVLQE------------EGNCTLCNNMCPN  198
         ||                    || :||| ||| |||:|             ||||| | | |
Db  170  GKKFIEGFQSTKLKDPRAQPGQSS-----PKIDVVISEASSSNNTLDPGTCTVFED---S  221

Qy  199  EVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----SPF  254
         |:             :| | |||   |||  ||::|| | |:|||| ||:|     |||
Db  222  ELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTVYLMDMCSFDTISTSTVDTKLSPF  281

Qy  255  CDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQQGVGYVNELLARLTGQAVRDETQTNRT  314
         |||||.:: :|| ||  | | |||| |||| ||:| || ||| ||||   :  ||: ||
Db  282  CDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHT   341

Qy  315  LDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD----SK  368
         |||.||||||| | ||||||||.  | :| || |  :    | ||   |: |||     |
Db  342  LDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSTTVENITQTDGFSSAW   399
```

```
Qy  369 LVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTYARE 424
            |||: :.:  |  | .::  ||||||||| |  |  |  |  |   :||    ::||
Db  400 TVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVRGLSFARS 458

Qy  425 NGQGDFAKC 433
            ||:|:|:|
Db  459 G--GDWAEC 465
```

Search completed: May 27, 2005, 08:30:24
Job time : 174 secs

```
                GenCore version 5.1.6
         Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      May 27, 2005, 08:27:27 ; Search time 40 Seconds
                                (without alignments)
                             1055.979 Million cell updates/sec

Title:       US-10-734-510-7
Perfect score: 2325
Sequence:    1 MVSSAFAPSILLSLMSSLAL.........TYARENGQGDFAKCGFVPSE 439

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_79:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	759.5	32.7	467	1	JN0656	3-phytase (EC 3.1.
2	754.5	32.5	467	1	JN0889	3-phytase (EC 3.1.
3	743.5	32.0	441	1	JN0482	3-phytase (EC 3.1.
4	412	17.7	463	2	S14119	acid phosphatase
5	390.5	16.8	463	2	T39929	thiamin-repressibl
6	390	16.8	453	2	A25326	acid phosphatase (
7	385	16.6	468	2	JC4285	acid phosphatase (
8	351	15.1	479	1	JN0715	3-phytase (EC 3.1.
9	348	15.0	479	1	JN0890	acid phosphatase (
10	345.5	14.9	467	1	PABYC	acid phosphatase (
11	335.5	14.4	467	1	PABYCC	acid phosphatase (
12	331.5	14.3	468	2	S52495	acid phosphatase h
13	315.5	13.6	467	2	S53476	acid phosphatase (
14	312.5	13.4	467	2	S48996	acid phosphatase (
15	162.5	7.0	468	2	A86233	hypothetical prote
16	159	6.8	465	2	JE0369	histidine acid pho
17	107.5	4.6	3972	2	S75251	hypothetical prote
18	104	4.5	2468	2	A83412	hypothetical prote
19	103.5	4.5	1250	2	D91018	hypothetical prote
20	103.5	4.5	1250	2	F85862	hypothetical prote
21	101.5	4.4	411	2	D88504	protein B0361.7 [i
22	101.5	4.4	1250	2	G64993	yfaL protein - Esc
23	101	4.3	438	2	S64682	acid phosphatase (
24	100	4.3	380	1	T16883	hypothetical prote
25	99	4.3	397	2	S52783	aspartic proteinas
26	99	4.3	415	2	T40535	probable arginine-
27	96.5	4.2	3623	2	T08618	intrinsic factor-B
28	95.5	4.1	604	2	H81110	sulfite reductase
29	95.5	4.1	770	2	S60676	cellobiose oxidase
30	95.5	4.1	926	2	D86897	hypothetical prote
31	95.5	4.1	1093	2	B86748	hypothetical prote
32	95	4.1	626	2	T41060	hypothetical ser-r
33	94.5	4.1	1335	2	H75511	DNA polymerase III
34	93.5	4.0	376	2	C84769	probable fibrillin
35	93	4.0	293	2	AB3051	hypothetical prote
36	93	4.0	300	2	B98235	fhuD protein (AJ00
37	93	4.0	401	2	T37132	probable hydrolase
38	93	4.0	408	2	T20893	hypothetical prote
39	93	4.0	533	2	AG2293	hypothetical prote
40	93	4.0	629	2	AE1525	probable peptidogl
41	93	4.0	1332	2	T23024	hypothetical prote
42	92.5	4.0	343	2	T09565	peroxidase (EC 1.1
43	92.5	4.0	1321	2	T51623	aldehyde oxidase (
44	92	4.0	508	2	S64958	aspartic proteinas
45	92	4.0	713	2	JE0230	NADPH-cytochrome P

ALIGNMENTS

```
RESULT 1
JN0656
3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger
N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C;Species: Aspergillus niger
C;Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0656; S28456
R;van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.I
A.M.J.
Gene 127, 87-94, 1993
A;Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)
A;Reference number: JN0656; MUID:9252284; PMID:8387447
A;Accession: JN0656
A;Molecule type: DNA
A;Residues: 1-467 <VAN>
A;Cross-references: UNIPROT:P34752; GB:Z16414; NID:g2392; PIDN:CAA78904.1; PID:g2393
A;Experimental source: strain NRRL3135
A;Note: parts of the sequence, including the amino end of the mature protein, were confi
C;Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and ino
C;Genetics:
A;Gene: phyA
A;Introns: 15/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-467/Product: 3-phytase A #status experimental <MAT>
F;27,59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #stat
F;81,361/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match             32.7%;  Score 759.5;  DB 1;  Length 467;
Best Local Similarity   38.2%;  Pred. No. 9.5e-54;
Matches  187;  Conservative  58;  Mismatches 161;  Indels  83;  Gaps  18;

Qy       2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPA-QNTSN------------------WGP 43
             ||:||      ||:
Db       3 VSAVLLPLYLL-------------SGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQ 50

Qy      44 YDPFFPV--EPYAAP--PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTD 99
            ||::| ||:          :: |||||||:     : |||||:|
Db      51 YAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFD 110

Qy     100 PKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDS 159
             |:|::| |:|:| :|  :|:: :|||:|:|||:|:|  ||
Db     111 GKYAFLKTYNYSLGADDLTPFGEQEJVNSGIKFYQRYESLTR-NIVPFIRSSGSSRVIAS 169

Qy     160 STNWTAGF------------GDASGETVLPTLQVVLQE------EGNCTLCNNMCPN 198
            |||:  ||          :||: |: |::|::|:         |
Db     170 GKKFIEGFQSTKLKDPRAQPGQSS-----PKIDVVISEASSSNNTLDPGTCTVFED---S 221

Qy     199 EVGDBSTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNA----SPF 254
            |:  : : |||:|||| :|          :|::|      |||||::| |:::  |||
```

Db   222 ELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDCSFDTISTSTVDTKLSPF 281
                ||||| ::|: :::: |||||||||||||||||||||||::|: |
Qy   255 CDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVYNELLARLTGQAVRDETQTNRT 314
                ||||||| :::|:: ||||||||||||||||||||| ||||||| :| |
Db   282 CDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHT 341
                ||||| ||||| ||||||||||||||||||||||||||||||||----SK 368
Qy   315 LDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD----SK 368
                ||| |||||||||||||||||||||||||||||||| :|:| |||||| |
Db   342 LDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSTTTVENITQTDGFSSAW 399
                |||||||| ||:||||| |: :|:: ||||| ||||||||||||| :|| |
Qy   369 LVPFSGHMTVEKLACSGKE--AVRLVNDAVQPLEFCGGVD--GVCELSAFVESQTYARE 424
                |||| | ::| | ||| :|||::| ||||:|: ::|
Db   400 TVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGC-PIDALGRCTRDSFVRGLSFARS 458
                |||||||||||| | ||| |
Qy   425 NGQGDFAKC 433
                ||:||:|:
Db   459 G--GDWAEC 465

RESULT 3
JN0482
3-phytase (EC 3.1.3.8) A - Aspergillus ficuum
N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C;Species: Aspergillus ficuum
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0482; PN0023
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 747-753, 1993
A;Title: Aspergillus ficuum phytase: Complete primary structure elucidation by chemical s
A;Reference number: JN0482; MUID:93249451; PMID:8387289
A;Accession: JN0482
A;Molecule type: protein
A;Residues: 1-441 <UL1>
A;Cross-references: UNIPROT:P34752
A;Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
R;Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 178, 45-53, 1991
A;Title: Cyclohexanedione modification of arginine at the active site of Aspergillus ficu
A;Reference number: PN0023; MUID:91299982; PMID:1648914
A;Accession: PN0023
A;Molecule type: protein
A;Residues: 48-70 <UL2>
C;Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate.
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;4,36,82,97,184,207,316,329,353,365/Binding site: carbohydrate (Asn) (covalent) #status
F;58,338/Active site: Arg, His #status predicted
F;59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match   32.0%;   Score 743.5; DB 1;   Length 441;
Best Local Similarity   40.4%;   Pred. No. 1.8e-52;
Matches 174; Conservative 53; Mismatches 151; Indels 53; Gaps 15;

Qy   41 WGPYDPFFPV--EPYAAP--PEGCTVTQVNLIQRHGARWPTSGARSRQVAVAVAKIQMARP 96
                  ||:|| || :|:||| |||||||||||||||||||| : |||||||||:::|
Db   25 WGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAT 84
Qy   97 FTDPKYEFLNDFVVKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRV 156
                  || |:: | ::|:| |||||:| ||||||||||||||||||||: ||||:||||||
Db   85 TPFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTR-NIVPFIRSSGSSRV 143
Qy   157 VDSSTNWTAGF------------GDASGETVLPTLQVVLQE------EGNCTLCNNM 195
                  |:|||||||| ||| ||||||:|::|:|| ||||:||||
Db   144 IASGKKFIEGFQSTKLKDPRAQPGQSS------PKIDVVISEASSSNNTLDPGTCTVFED- 197
Qy   196 CPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDCPFDTLSSGNA---- 251
                     :::: :|| |:|||| : ::|: :::
Db   198 --SBLADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDCSFDTISTSTVDTKL 255
Qy   252 SPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVYNELLARLTGQAVRDETQT 311
                  ||||||:| |||||||||||:|:: :||||||||| |||||||:||||| :|| :|
Db   256 SPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSS 315
Qy   312 NRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPD--ENRLWVD--- 366
                  | |||| ||||| | |||||||| |: :|:: ||||| |||||||| |
Db   316 NHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSTTTVENITQTDGFS 373

```
Qy    367  -SKLVPFSGHMTVEKLACSGKE--AVRVLVNDAVQPLEFCGGVD--GVCELSAFVESQTY 421
           ||||||||||||||||  ::     ||||||  |:  ||    :: ||
Db    374  SAWTVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGC-PVDALGRCTRDSFVRGLSF 432

Qy    422  ARENGQGDFAK 432
           ||  ||:|:
Db    433  ARSG--GDWAE 441

RESULT 4
S14119
acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S14119; T40455
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
R;Yang, J.; Schweingruber, M.E.
Curr.Genet. 18, 269-272, 1990
A;Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosa
A;Reference number: S14119; MUID:91064763; PMID:2249257
A;Accession: S14119
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-463 <YAN>
A;Cross-references: UNIPROT:Q01682; GB:X56939; NID:g5006; PIDN:CAA40258.1; PID:g5007
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21931
A;Accession: T40455
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-463 <LYN>
A;Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c
A;Experimental source: strain 972h-; cosmid c428
C;Genetics:
A;Gene: SPBC428.03c
A;Map position: 2
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase

Query Match             17.7%;      Score 412;      DB 2;      Length 463;
  Best Local Similarity   32.6%;      Pred. No. 1.5e-25;
  Matches  141;  Conservative  58;  Mismatches  168;  Indels  66;  Gaps   22;

Qy     44  YDPFFVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMAR--------- 95
           ::||:|  ||||||||||:|||||||||||:|||:  |  :|:
Db     43  HEPYFN-GPTTSFPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQYIDIFQNKLLNGSI 101

Qy     96  PFT-----DPKYEFLNDF--VYKFGVAD-LLPFGANQSHQTGTDMYTRYSTLFEGGDVPF 147
            ||       ||||||||    ||||| ||||:|||   | ||||||||||||||||||
Db    102  PVNFSYPENPLY-FVKHWTPVIKAENADQLSSSGRIELFDLGRQVFERTYELFD-TDVTD 159

Qy    148  VRAAGDQRVVDSSTNWTAG-FGDASGETVLPTLQVVLQEB---GNCTLCNNMCPNEVDG 202
           ||||||||||||||||||| |||||||||||||||||| :   | ||  |: |  | 
Db    160  INTAAQERVVDSAEWFSYGMFGD---DMQNKTNFIVLPEDDSAGANSLAMYYSCPVYEDN 216

Qy    203  --DSTT------WLGVFAPNITARLNAAAPSA-NLSDSDALTLMDCPFDTLSSGNASP 253
             :|||       ||||||||||||||||| || :||| |  ||  || ||||| |
Db    217  NIDENTTEAAHTSWRNVFLKPIANRLNKYFDSGVNLTVSDVRSLYYICVYEIALRDN-SD 275

Qy    254  FCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVGVNELLARLLTGQAVRDETQTNR 313
           |  |||||||||  ::::|||||   |||||||  |  |||| ||| ||
Db    276  FCSLFTPSEFLNFEYDSDLDYAYWGGPASEWASTLGGAVNNLANNL--------RKGVNN 328

Qy    314  TLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLF-NATALDPLKPDENRLWVD---SKL 369
            |||||||||||||||||||||||||||||||||| |||||||||||||||:||   :||
Db    329  ASD--------RKVFLAFTHDSQIIPVEAALGFFPDITPEHPLPTDKNIFTYSLKTSSF 379

Qy    370  VPFSGHMTVEKLACS-GKEAVRVLVNDAVQPLEFC----GGVDGVCELSAFVES--QTY 421
           |||||||||||||| ||||||||||||||||||||    ||:| ||| |||||   |||
Db    380  VPFAGNLITELFLCSDNKYYVRHIVNQQVYPLTDCGYGPSGASDGLCELSAYLNSSVRVN 439

Qy    422  ARENGQGDF-AKC 433
```

```
Db    440  STSNGIANFNSQC 452
           ||  | ::|  ::|

RESULT 5
T39929
thiamin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39929
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21857
A;Accession: T39929
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-463 <LYN>
A;Cross-references: UNIPROT:O60172; EMBL:AL023286; PIDN:CAA18863.1; GSPDB:GN00067; SPDB:S
A;Experimental source: strain 972h-; cosmid c21H7
C;Genetics:
A;Gene: SPDB:SPBC21H7.03c
A;Map position: 2
C;Superfamily: yeast acid phosphatase

Query Match             16.8%;      Score 390.5;      DB 2;      Length 463;
  Best Local Similarity   28.4%;      Pred. No. 8.4e-24;
  Matches  127;  Conservative  60;  Mismatches  161;  Indels  99;  Gaps   18;

Qy     42  GPYDPFFVEBPY-----AAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARP 96
           ||  ||||| ||      :  :|||:|||||||||||| ||||||:||:: |  |
Db     37  GTLSPYH--EPYFDGLDSAFPETCEIQQVHLLQRHGSRNPTGDVIATDVYS-------- 85

Qy     97  FTDPKYEFLNDFVYKF------------------GVADLLPFGANQSHQ 127
            :||||  |:  : |:                  |||  ||||||:|||
Db     86  -----SQYLNNFQBKLLNGSIPVNFSYPENPLCFIKQWTPVIDAENADQLSSSRGRLEFD 140

Qy    128  TGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAG-FGDASGETVLPTLQVVLQEB 186
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    141  LGRQLYQRYYKLFD-SYVVDINTAEQERVVESAKWFTYGLFGDKMYEKT----NFILISE 195

Qy    187  GNCTLCN-------NMCP------------NEVDGDESTTWLGVFAPNITARLNAAAPSA-NLSD 231
           | ||  |       |  |             |   |:| | ||||||||||||| | ||
Db    196  GKAAGANSLSMYNACPVFKDNNFHKNATDAAHA-VWRNIFIEPIVNLRAKYFDSSYKLTI 254

Qy    232  SDALTLMDCPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGVG 291
           ||| |||  || ||||| |||| | :: || ||   :|:|||  | |||| |  |  |
Db    255  NDVRSLFYICEYE-IAIKDHSDFCSIFTPSEFLNFEYDSDLDQAYGGGPVSEWASTLGGA 313

Qy    292  YVNELLARLTGQAVRDETQTNRTLSDPATFPLNRTFYADFSHDNTMVPIFAALGLF-NA 350
           |||| |||| |  | |:|    |||||||||||||||||||||||||||||||||| ||
Db    314  YINNL-----ADSLRNVTNPD-----------FDRKVFLAFTHDSNIIPVEAALGFFPDI 357

Qy    351  TALDPLKPDENRLWVDSK---LVPFSGHMTVEKLACS-GKEAVRVLVNDAVQPLEFC--- 403
           |||||||||||||||  |   ||||||||||||||| ||||||||||||||||||
Db    358  TPQNPLPTDKNIYTYSQKTSSFVPFAGNLITELFFCSDSKYYVRHIVNQQVYPLIDCGYG 417

Qy    404  --GGVDGVCELSAFVESQTYARENGQQ 428
             |||| ||| ||| |  ||:|:  |:
Db    418  PSGTSDGLCELQAYLNSPIRANSTSNG 444

RESULT 6
A25326
acid phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharomyce
C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25326; T50405
R;Elliott, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J.
J. Biol. Chem. 261, 2936-2941, 1986
A;Title: Isolation and characterization of the structural gene for secreted acid phosphat
A;Reference number: A25326; MUID:86140050; PMID:3005272
A;Accession: A25326
A;Molecule type: DNA
```

A;Residues: 1-453 <ELL>
A;Cross-references: UNIPROT:P08091; GB:M11857; NID:g173422; PIDN:AAA35321.1; PID:g173422
R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25068
A;Accession: T50405
A;Molecule type: DNA
A;Residues: 1-453 <RIE>
A;Cross-references: EMBL:AL137099; PIDN:CAB68657.1; GSPDB:GN00067; SPDB:SPBP4G3.02
A;Experimental source: strain 972h(-); clone p1 p4G3
C;Genetics:
A;Gene: pho1; SPDB:SPBP4G3.02
A;Map position: 2
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;68/Active site: Arg #status predicted
F;69/Active site: His (phosphohistidine intermediate) #status predicted

```
Query Match     16.8%;  Score 390;  DB 1;  Length 453;
Best Local Similarity   29.7%;  Pred. No. 8.9e-24;
Matches 138;  Conservative  58;  Mismatches 190;  Indels  78;  Gaps  22;

Qy      6 FAPSILLSMSSLALSTQFS-FVA--AQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTV 62
            :|| :||| ||| ||||:||     |:|| |||||||||||||||||||||||||||
Db      2 FLQNLFLGFLAVVCANAQFAEFTAFDGKFDFKEHLTSRSPYHKPYF-YGPSIDFPTTCKI 60

Qy     63 TQVNLIQRHGARWPTSGARSRQVAAVAKIQMAR--------------PFTDPKYE 103
            :|||||||||||||:||||||||||||||||              |||||||
Db     61 KQVHTLQRHGSRNPTGGNAAFDAVGIANFQQRLLNGSVPIDYSVSGNPLSFVPTWTPVIE 120

Qy    104 FLNDFVYKFGVADLL-PFGANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTN 162
            |||||||||  :|     | |||||||||||||:  ||||||||||||  |||||||:
Db    121 AAN-------ADALSSSGRVELFDMGRQFYERYHELFNASTNIYTRA-QQRVVDSAL- 170

Qy    163 WTAGFGDASGETVLPTLQVVLQEE----GNCTLCNNMCPNEVDGDESTT-----WLGVF 212
            |||||||||||||||||||||||    |||||||||||||  | :::       ||||
Db    171 W-YGYG-MFGEDVHNFTNYILVSENATAGSNSLSSYNACPAS-DADDFTTPALEAWRNVY 227

Qy    213 APNTARLNAAAPSANLSDSDALTLMDCPFDTLSSGNASPFCDLFTABEYVSYEYYYDL 272
            |||:||||||||||||||||||||||||||||||||||:  ||  |||: ::: ||
Db    228 MPPIRQRLNPYFSNYNLTNDDILNLYGICSYE-IALQDYSEFCKLFNSVDFLNFEYEGDL 286

Qy    273 DKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADF 332
            |||||||||||| :::||| ::||||||||  ||||||||||||||||||||||||||
Db    287 SFSYGMGNSVKWGSIFGGAYANSLANSL--RSVENNTQ-------QVFFA-F 328

Qy    333 SHDNTMVPIFAALGLF-NATALDPLKPD----ENRLWVDSKLVPSGHMTVEKLAC-SGKE 387
            :||:||| ||||||||     ||||||||    :|| |||||||||||||||||:   :||
Db    329 THDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMKASEFVPFAGNLITELFQCEDDSKY 388

Qy    388 AVRVLVNDAVQPLEFCG-------GVDGVCELSAFVESQTYARENG 426
            |:|:|||||| ||:|:       ||  |||  ||:|| |||
Db    389 YVRHLVNEEVFPLSDCGFGPSNVTSDGMCELYAYLNSP--VRVNG 430
```

RESULT 7
JC4285
acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)
N;Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
C;Species: Pichia pastoris
C;Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4285
R;Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A;Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterization
A;Reference number: JC4285; MUID:96001238; PMID:7555473
A;Accession: JC4285
A;Molecule type: DNA
A;Residues: 1-468 <PAY>
A;Cross-references: UNIPROT:P52291; GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A;Experimental source: GS115
C;Genetics:
A;Gene: pho1

C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-468/Product: acid phosphatase #status predicted <MAT>
F;84/Active site: His (phosphohistidine intermediate) #status predicted
F;163,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;345/Active site: His #status predicted

```
Query Match     16.6%;  Score 385;  DB 2;  Length 468;
Best Local Similarity   29.4%;  Pred. No. 2.4e-23;
Matches 143;  Conservative  61;  Mismatches 192;  Indels  90;  Gaps  23;

Qy      6 FAPSILLSMSSLALSTQFSFVAAQL---------PIPAQNTSNWGPYDPFFPVEPY--- 53
            |:| :|||  ||:||| ||                 |  |||||||||||||||||
Db      2 FSP--ILSLEIILALATLQSVFAVBLQHVLGVNDRPYPQRTDDQYNILRHLGGLGPYIGY 59

Qy     54 -------AAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMA--RPFTDPKYEF 104
                   ||  |:  || ||||||||||||||||||||||||||||   |||||||
Db     60 NGWGIAAAESEIESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGP-LSF 118

Qy    105 LNDFVYKFGVADLLPF---------GANQSHQTGTDMYTRYSTLF-EGGDVPFVRAA 151
            |||| ||||  ||             ||| ||||||||||| |:  |||||||||||
Db    119 FQD--YDYFVSDAAWYEQETTKGFYSGLNTAFDFGTTLRRERYDHLINTSEGGKKLSVWAG 176

Qy    152 GDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEG---NCTLCNNMCPN-----EVDG 202
            ||||||||||||||||||||||||||||||||      ||:|||||||      ||
Db    177 SQERVVDTAKYFACGFMKSNYTDMEV--VALEEKSQGLNSLTARISCPNYNSHIYKDG 234

Qy    203 DESTTWLGVFAPNITA-------RLNAAAPSANLSDSDALTLMDCPFDTLSSGNASPFCDL 257
            |||| ||||| |:          ||:||:||||||||||||||||||||||||||||:
Db    235 D------FPNDIAEREADRLNTLSPGFNITADDIPTIALYCGFELNVRGESS-FCDV 284

Qy    258 FTABEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDS 317
            |||:|||: ||| ::                 :|| ||||||||||:       ||
Db    285 LSRBALLYTAYLRDLGWYNVGNGNPLGKTIGYVYAN--------ATR---QLLENTEA 332

Qy    318 DPATFPLNRTFYADFSHDNTMVPIFAAGLFNATALDPLKPDENRLWVDSKLVPSGHMT 377
            ||||||||| :|||| :: ||| ||||||||||| ||||:|||||||||||||||||
Db    333 DPRDYPL---YFSFSHDTDLLQVFTSLGLFNVTDLPLDQIQFQTSFKSTEIVPMGARLL 388

Qy    378 VEKLACS--GKEA--VRVLVNDAVQPLEFCGGGVDGV-CELSAFVESQTYARENGQGDFAK 432
            ||:|| |  |:      ||||||||||||||| | ||  ||:| ||: :|| ::|
Db    389 TERLLCTVBGEEKYYVRTILNDAVFPLSDCSSGGFSCPLNDYVSRLEALNED--SDFAE 446

Qy    433 -CGFVP 437
            :||||
Db    447 NCG-VP 451
```

RESULT 8
JN0715
3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficuum
N;Alternate names: pH 2.5-optimum acid phosphatase
C;Species: Aspergillus ficuum
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
R;Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 195, 53-57, 1993
A;Title: Identification and cloning of a second phytase gene (phyB) from Aspergillus nige
A;Reference number: JN0715; MUID:93371452; PMID:7916610
A;Accession: JN0715
A;Molecule type: DNA
A;Residues: 1-479 <EHR>
A;Cross-references: UNIPROT:P81440; GB:L20567
A;Accession: PN0594
A;Molecule type: protein
A;Residues: 20-101;133-146;376-399 <EH2>
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A;Title: Identification of active-site residues in Aspergillus ficuum extracellular pH 2.
A;Reference number: PN0460; MUID:93249452; PMID:8484781
A;Accession: PN0460
A;Molecule type: protein

```
A;Residues: 65-66,68-93 <ULL>
C;Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), hy
C;Genetics:
A;Gene: phyB
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status experimental <MAT>
F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match             15.1%;    Score 351;  DB 1;   Length 479;
Best Local Similarity   27.9%;    Pred. No. 1.4e-20;
Matches 131;  Conservative 68;  Mismatches 157;  Indels 114;  Gaps 24;

Qy      11 LLSLMSSLAL-STQFSFVAAQLPIPAQN-----------TSNWGPYDPFFPVEPYAA- 55
           ||:|| :|:|| :: ||:|| |:|                    ::|:|
Db       6 LLTLACALATGASAFSYGAA-IPQSTQEKQFSQEFRDGYSILKHYGGNGPYSERVSYGIA 64

Qy      56 --PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYE--FLNDFVYK 111
            ||:|||:| ||::|||||:||||||:||:| : :| |: ::|    ::| | |||||
Db      65 RDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINT-TEYKGDLAFLNDWTY- 122

Qy     112 FGVADLLP-----------------------FGANQSHQTGTDMYTRYSTLFEGGD-VPFVRAAGDQRV 156
           |||||||                          ||      :: :|||| |||:| |||||||:|||
Db     123 -----YVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPFF-SSGYGRV 176

Qy     157 VDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPN-EVDGDESTTWLGVFAPN 215
           |:::: :| |||:| :|  |:|    :|    :||:|:| ||:|:::::| |:||:|
Db     177 IETARKFGEGF---FGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTT------CDN 227

Qy     216 IT--------ARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPF---CDLFTAEE 262
           |:         |:||||:| :||::|||||||||||||||||  ||   |||||||
Db     228 LTYQLPQFKVAAARLNSQNPGMNLTASDVVNLMVMASFEL----NARPFSNWINAFTQDE 283

Qy     263 YVSYEYYYDLDKYYGTGPGNALGPVQGVGVYNELLARLTGQAVRDETQTNRTLDSDPATF 322
           ::|||:|:||:| ||  |||:  |:|||:| :||||||||:| |:| :
Db     284 WVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLT-LLNQGPKRA-------------- 328

Qy     323 PLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVD---------SKLVPF 372
           ||||:|||||||||||||:|||||||||||||:||:  |||||   |||:||:
Db     329 --GSLFFNFAHDTNITPILAALGV-------LIPNED-LPLDRVAFGNPYSIGNIVPM 376

Qy     373 SGHMTVEKLACSGKEA--------VRVLVNDAVQPLEFCGGVDGV-CELSAF 415
           |||||:| :|::|:|           ||:|:||||||:||| ||  ||||:
Db     377 GGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDCTSGPGYSCPLANY 426
```

```
RESULT 9
JN0890
acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0890
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
A;Reference number: JN0889; MUID:94040796; PMID:8224894
A;Accession: JN0890
A;Molecule type: DNA
A;Residues: 1-479 <PID>
A;Cross-references: UNIPROT:P34755; GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A;Experimental source: strain ALKO243
C;Comment: The highly similar enzyme from A. ficuum has been shown to have 3-phytase (EC
C;Genetics:
A;Gene: aph
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status predicted <MAT>
```

```
F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match             15.0%;    Score 348;  DB 1;   Length 479;
Best Local Similarity   27.2%;    Pred. No. 2.5e-20;
Matches 128;  Conservative 70;  Mismatches 158;  Indels 114;  Gaps 23;

Qy      11 LLSLMSSLAL-STQFSFVAAQLPIPAQN-----------TSNWGPYDPFFPVEPYAA- 55
           ||:|| :|:|| :: ||:|| |:|                    ::|:|
Db       6 LLTLACALATGASAFSYGAA-IPQSTQEKQFSQEFRDGYSILKHYGGNGPYSERVSYGIA 64

Qy      56 --PPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYE--FLNDFVYK 111
            ||:|||:| ||::|||||:||||||:||:| : :| |: ::|    ::| | |||||
Db      65 RDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINT-TEYKGDLAFLNDWTY- 122

Qy     112 FGVADLLP-----------------------FGANQSHQTGTDMYTRYSTLFEGGD-VPFVRAAGDQRV 156
           |||||||                          ||      :: :|||| |||:| |||||||:|||
Db     123 -----YVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPFF-SSGYGRV 176

Qy     157 VDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPN-EVDGDESTTWLGVFAPN 215
           |:::: :| |||:| :|  |:|    :|    :||:|:| ||:|:::::| |:||:|
Db     177 IETARKFGEGF---FGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTT------CDN 227

Qy     216 IT--------ARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPF---CDLFTAEE 262
           |:         |:||||:| :||::|||||||||||||||||  ||   |||||||
Db     228 LTYQLPQFKVAAARLNSQNPGMNLTASDVVNLMVMASFEL----NARPFSNWINAFTQDE 283

Qy     263 YVSYEYYYDLDKYYGTGPGNALGPVQGVGVYNELLARLTGQAVRDETQTNRTLDSDPATF 322
           ::|||:|:||:| ||  |||:  |:|||:| :||||||||:| |:| :
Db     284 WVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLT-LLNQGPKRA-------------- 328

Qy     323 PLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVD---------SKLVPF 372
           ||||:|||||||||||||:|||||||||||||:||:  |||||   |||:||:
Db     329 --GSLFFNFAHDTNITPILAALGV-------LIPNED-LPLDRVAFGNPYSIGNIVPM 376

Qy     373 SGHMTVEKLACSGKEA--------VRVLVNDAVQPLEFCGGVDGV-CELSAF 415
           |||||:| :|::|:|           ||:|:||||||:||| ||  ||||:
Db     377 GGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDCTSGPGYSCPLANY 426
```

```
RESULT 10
PABYC
acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
C;Species: Saccharomyces cerevisiae
C;Date: 19-Feb-1984 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S05795; A38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A27.
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A;Reference number: S05794; MUID:85037940; PMID:6093051
A;Accession: S05795
A;Molecule type: DNA
A;Residues: 1-467 <BAJ>
A;Cross-references: UNIPROT:P00635; EMBL:X01079; NID:g4162; PIDN:CAA25555.1; PID:g758282
A;Note: the authors translated the codon TAC for residue 272 as Thr
A;Accession: A38792
A;Molecule type: protein
A;Residues: 18-45 <BAJ2>
R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:7900426
A;Accession: S48260
A;Molecule type: DNA
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-467 <MAN>
A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55598.1; PID:g476051
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
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A;Accession: S45961
A;Molecule type: DNA
A;Residues: 1-467 <FE2>
A;Cross-references: EMBL:Z35962; NID:g536364; PIDN:CAA85046.1; PID:g536365; GSPDB:GN0000
R;Arima, K.; Oshima, T.; Kubota, I.; Nakamura, N.; Mizunaga, T.; Toh-e, A.
Nucleic Acids Res. 11, 1657-1672, 1983
A;Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repres
A;Reference number: A00777; MUID:83168913; PMID:6300772
A;Accession: A00777
A;Molecule type: DNA
A;Residues: 1-35,'Y',37-129,'G',131-293,'Q',295-445,'V',447-461,'DT',464-465,'K',467 <AR
A;Cross-references: EMBL:V01320; NID:g4158; PIDN:CAA24630.1; PID:g4159
A;Accession: A38793
A;Molecule type: protein
A;Residues: 18-26,'X',28 <ARI2>
R;Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinnen, A.
EMBO J. 1, 675-680, 1982
A;Title: Two yeast acid phosphatase structural genes are the result of a tandem duplicat
A;Reference number: S41855; MUID:84236032; PMID:6329697
A;Accession: S41855
A;Molecule type: DNA
A;Residues:1-30,'T',32-51,'S',53-75 <MEY>
A;Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
R;Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G
Mol. Cell. Biol. 6, 1855-1865, 1986
A;Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A;Reference number: A93074; MUID:87064474; PMID:3537710
A;Accession: B25241
A;Molecule type: DNA
A;Residues: 1-44 <TAI>
A;Accession: A27774
R;Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A;Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A;Reference number: A25367; MUID:87064526; PMID:3023927
A;Accession: A25367
A;Molecule type: DNA
A;Residues: 1-2,'Y',4-43,'T',45-51 <BER>
R;Silve, S.; Monod, M.; Hinnen, A.; Haguenauer-Tsapis, R.
Mol. Cell. Biol. 7, 3306-3314, 1987
A;Title: The yeast acid phosphatase can enter the secretory pathway without its N-termin
A;Reference number: A27774; MUID:88038886; PMID:3313013
A;Accession: A27774
A;Molecule type: DNA
A;Residues: 1-51,'S',53-60 <SIL>
A;Cross-references: GB:M17306
C;Genetics:
A;Gene: SGD:PHO5; MIPS:YBR093c
A;Cross-references: SGD:S0000297; MIPS:YBR093c
A;Map position: 2R
A;Note:YBR093c
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase, repressible #status experimental <MAT>
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval
F;337/Active site: His #status predicted

Query Match   14.9%;   Score 345.5;   DB 1;   Length 467;
Best Local Similarity   27.5%;   Pred. No. 3.8e-20;
Matches 122;   Conservative   59;   Mismatches 158;   Indels 105;   Gaps 21;

Qy   42 GPYDPFFVEPYAAP---------PEGCTVTQVNLIQRHGARWPT-SGARSRQVAAVAKI 91
                |||| ||:|| ||||| ||||| :: :||
Db   45 GPY------YSFPGDYGISRDLPEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLS 96

Qy   92 QMARPFTDPKYEFLNDFVYKFGVAD-------------LLPF-GANQSHQTGTDMYT 134
                :|| |||| |||| || :| :   : :
Db   97 NYTRQF-NGSLSFLND-DYEFFIRDDDDLEMETTFANSDDVLNPYTGEMNAKRHARDFLA 154

Qy   135 RYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEE--GNCTL- 191
                : ||| :: ||| : || | :| | |: : | | ::
Db   155 QYGYMVENQTSPAVFTSNSKRCHDTAQYFIDGLGDQFN----ITLQTVSEAESAGANTLS 210

Qy   192 -CNNMCP--------NEVDGESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPF 243
                  ::: ||| | : | : || ::
Db   211 ACNS-CPAWDYDANDDIVNEYDTTYL---DDIAKRLNKENKGLNLTSTDASTLFSWCAF 265

Qy   244 DTLSGSGNASPFCDLFTAEEVSYEYYYDLDKYYGYGTGPGNALGPVQGVGYVNELLARLTGQ 303
                ||||| : ||::|| || :   : | | :|| :||
Db   266 EVNAKG-YSDVCDIFTKDELVHYSYYQDLHTYYHEGPGYDIIKSVGSNLFNASVKLLKQS 324

Qy   304 AVRDETQTNRTLDSDDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRL 363
                :   :::| | | || ||
Db   325 BIQDQ--------------KVWLSFTHDTDILNFLTTAGIID--------DKNNL 357

Qy   364 WVDSKLVPFSGH-----------MTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGV- 409
                                       ::| ::   : : : | : |
Db   358 --TAEYVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYIVNDAVVPIETCSTGPGFS 415

Qy   410 CELSAFVESQTYARRNGQG-DFAK 432
                |||| : ||:
Db   416 CEINDFYD---YAEKRVAGTDFLK 436

RESULT 11
PABYCC
acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (Saccharomyces cerevisiae)
N;Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S48259; S45960; S05794; A25241; S44674
R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:790426
A;Accession: S48259
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-467 <MAN>
A;Cross-references: UNIPROT:P24031; EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476045
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
A;Accession: S45960
A;Molecule type: DNA
A;Residues: 1-467 <FE2>
A;Cross-references: EMBL:Z35961; NID:g536361; PIDN:CAA85045.1; PID:g536363; GSPDB:GN0000
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A;Reference number: S05794; MUID:85037940; PMID:6093051
A;Accession: S05794
A;Molecule type: DNA
A;Residues: 1-218,'MKT',222-467 <BAJ1>
A;Cross-references: EMBL:X01080; NID:g4148; PIDN:CAA25557.1; PID:g758281
A;Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue 2
R;Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A;Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within t
A;Reference number: A93074; MUID:87064474; PMID:3537710
A;Accession: A25241
A;Molecule type: DNA
A;Residues: 1-44 <TAI>
C;Genetics:
A;Gene: SGD:PHO3; MIPS:YBR092c
A;Cross-references: SGD:S0000296; MIPS:YBR092c
A;Map position: 2R
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolas
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97,103,162,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (covale
F;337/Active site: His #status predicted

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Query Match     14.4%;     Score 335.5;  DB 1;  Length 467;
Best Local Similarity     26.3%;     Pred. No. 2.5e-19;
Matches 124;   Conservative 63;   Mismatches 186;   Indels  99;   Gaps  19;

Qy    21 STQSFVAAQL----PIP---AQNTSNWGPYDPFFVEPYAAP-----------PEG  59
            :  | |||  |         ||          |||||  |||||           |||
Db     4 SVVYSVLAALVNAGTIPLGELADVAKIGTQEDIPFFLGGAGPYSFPGDYGISRDLPEG  63

Qy    60 CTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYSKYEFLNDFVYKFGVAD 116
         |||  |  | ||||| |     |  | |       |    |      | :||||  :
Db    64 CEMKQLQMLARHGERYPYTSKGATIMKTWYKLSNYTRQFNGSLSFLND-DYEFFIRDDDD 122

Qy   117 ----LLPF-GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTN 162
             |||| |||||| ||||||||||||||||||||||||||
Db   123 LEMETTPANSDNVLNPYTGEMDAKRHAREFPLAQYGYMFENQTSPPIFAASSERVHDTAQY 182

Qy   163 WTAFGFGDASGETVLPTLQVVLQEEGNCTLCNNMCP--NEVDGDE-----STTWLGVFAPN 215
              || |||| ||    |  |  |  |     |||  ::       |        ||   |:|
Db   183 FIDLGLGDQFNIS-LQTVSEAMSAGANTLSAGNACPGWDEDANDDILDKYDTTYL----DD 237

Qy   216 ITARLNAAPSANILSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEVVSYEYYYDLDKY 275
         | ||||  ::| :|: ||||  | |  | |   |  | ||| | :|  ||:|| |||  |
Db   238 IAKRLNKENKGLNLTSKDANTLFAWCAYE-LNARGYSDVCDIFTEDELVRYSYGQDLVSF 296

Qy   276 YGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHD 335
         | :||| |   : |||   :|    |      | | |    | ||||||
Db   297 YQDGPGYDMIRSVGANLFNATLKLLK---QSETQDLKV--------------WLSFTHD 338

Qy   336 NTMVPIFAALGLFNATALDLPLKPDENRLWDSKLVPFSGH-----------MTVEKLA 382
           :  |:     |  :  |            |      ||| |           :||
Db   339 TDILNYLTTAGIID----------DKNNL--TAEVVPFMGNTFHKSWYVPQGARVYTEKFQ 387

Qy   383 CSGKEAVRVLVNDAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG-DPAK 432
         |      || | ||| | |  |  |  |  |||| | ||| ||    : :|
Db   388 CSNDTYVRVVINDAVVPIETCSTGPGFSCEINDFYD---YABKRVAGTDFLK 436
```

RESULT 12
SS2495
acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2815
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: SS2495; S67556
R;Andre, B.; Vissers, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV
A;Reference number: SS2492
A;Accession: SS2495
A;Molecule type: DNA
A;Residues: 1-468 <URR>
A;Cross-references: UNIPROT:P52290; EMBL:Z48432; NID:g683669; PIDN:CAA88335.1; PID:g6836
A;Experimental source: strain S288C
R;Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67535
A;Accession: S67556
A;Molecule type: DNA
A;Residues: 1-468 <AND>
A;Cross-references: EMBL:Z74072; NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MIPS:YDL02
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD;DIA3
A;Cross-references: SGD:S0002182
A;Map position: 4L
C;Superfamily: yeast acid phosphatase

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Query Match     14.3%;     Score 331.5;  DB 2;  Length 468;
Best Local Similarity     27.8%;     Pred. No. 5.2e-19;
Matches 128;   Conservative 59;   Mismatches 198;   Indels  75;   Gaps  23;

Qy     9 SILLSLMSSLALSTQF-SFVAAQLPIPAQNT-----SNWGPYDFFFVBPYAAP---PEG  59
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RESULT 13
S53476
acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAR071w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S53476; JC1018
R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabach
submitted to the EMBL Data Library, February 1994
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 5:
A;Reference number: S53458
A;Accession: S53476
A;Molecule type: DNA
A;Residues: 1-467 <BUS>
A;Cross-references: UNIPROT:P35842; EMBL:L28920; NID:g1616966; PIDN:AAC09508.1; PID:g4561
R;Chen, J.Y.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A;Title: The primary structure of acid phosphatase gene PHO11 in S. cerevisiae and compa1
A;Reference number: JC1018
A;Accession: JC1018
A;Molecule type: DNA
A;Residues: 1-16, 'L',18-149,'H',151-353,'Q',355-422,'G',424-467 <CHE>
A;Note: this paper is in Chinese, with an English abstract
C;Genetics:
A;Gene: SGD:PHO11
A;Cross-references: SGD:S0000094; MIPS:YAR071w
A;Map position: 1R
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola:
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase #status predicted <MAT>
F;74/Active site: Arg #status predicted
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97,162,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status

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Query Match     13.6%;     Score 315.5;  DB 2;  Length 467;
Best Local Similarity     24.1%;     Pred. No. 1e-17;
Matches 115;   Conservative 67;   Mismatches 195;   Indels 101;   Gaps  17;

Qy     1 MVSSAFAPSILLLSMSSLALSTQ-FSFVAAQLPIPAQNTSNWGPYDPFFPVBPYAAP---  56
          :|:::          ||| |||  ||         ||||                |:  |
Db     8 AICLGVLLSKALSIPLRSFADIEL-IGSQKSLFFPLGGSAPYFS-FPAN-YGIPTDIPEG  64

Qy    60 CTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYE---FLNDFVYKFGVA 115
         | :|||  | |||| |   : :   |   :  |    |  |         ||:  ||||
Db    65 CRLTQVQMIGRHGERYPTRSEAKDIFEVWYKIS---NYTG-KYEGGSLSFLNN-GYEFFIP 119

Qy   116 D------LLPF-GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVD 158
         |       | :     :    ||   |          |      |
Db   120 DESLLEMETTLQNSIDVLNPYTGEMNAKRHAREFLAKYGKLMENCTNFPIFTTNSKRIYD 179

Qy   159 SSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPN---EVDGDESTTWLGVFAPN 215
           :     | ||  |   |  |   |  |     ||  |        :      || |
Db   180 TAQYFAEALGDGFNIS-LQTLSENSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLEN 238

Qy   216 ITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTABEYVSYEYYYDLDKY 275
         |: ||| : ::  |  ||| |  | |  |      |    ||| | :|  ||:|| |
Db   239 ISDRLNDENKGLNLSRKDAAALFSWCAFE-LNAKGYSNICDIFSAAELIHYSYETDLTSF 297

Qy   276 YGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHD 335
         | :||| |   : |||   :|    :        | | |    | ||||
Db   298 YQNGPGYKL--IKSIG------ANLFNATVKLIRQSAH-------LDQKVWLSFTHD 339

Qy   336 NTMVPIFAALGLFN----ATALDPLKPDE-NRLWDSKLVPFSGHMTVEKLACSGKEAV 389
           :  |:     |        |          |      ||| |:||::|
Db   340 TDILNYLTTAGLIDDTRNLTTNHVFRDHSYHRSW---YIPQGARVYTEKFQCSNDSYV 395

Qy   390 RVLVNDAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG 428
         |  | ||| | |  |  |  |  |||  | ||| |
Db   396 RYVVNDAVVPIESCSSGPGFSCEEGTFYE---YAKDRLRG 432
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Db   :|:.| EFFIRDTKNLEMETTLANSVNVLNPYTGEMNAKRHARDFLAQYGMVENQTSFAVFTSNS 173

Db 114 EFFIRDTKNLEMETTLANSVNVLNPYTGEMNAKRHARDFLAQYGMVENQTSFAVFTSNS 173

Qy 154 QRVVDSSTNWTAGFGDASGETVLPTLQVVLQEE---GNCTLCNNMCP---NEVDGDESTT 207

Db 174 NRCHDTAQYFIDGLGDKFN----ISLQTISEAESAGANTLSAHHSCPAWDDDVNDDILKK 229

Qy 208 WLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYE 267

Db 230 YDTKYLSGIAKRLNKENKGLNLTSSDANTFFAWCAYE-INARGYSDICNIFTKDELVRFS 288

Qy 268 YYYDLDKYYGTGPGNALGPVQGVGVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRT 327

Db 289 YGQDLETYYQTGPGYDVVRSVGANLFNASVKLLKESEVDQ----------------K 330

Qy 328 FYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVD---------SKLVPFSGHM 376

Db 331 VWLSFTHDTDILNYLTTIGIID--------DQNNLTAEHVPFMENTFHRSWYVPQGARV 381

Qy 377 TVEKLACSGKEAVRLVNDAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG-DFAK 432

Db 382 YTEKFQCSNDTYRYVRYVINDAVVPIETCSTGPGFSCEINDF---YGYAEKRVAGTDFLK 436

RESULT 15
A86233
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86233
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khayin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <STO>
A;Cross-references: UNIPROT:O04509; GB:AE005172; NID:g2160177; PIDN:AAB60740.1; GSPDB:GN(
C;Genetics:
C;Map position: 1
C;Superfamily: yeast acid phosphatase

Query Match   7.0%;   Score 162.5;   DB 2;   Length 468;
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Qy   57 PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVA------KIQMARPFTDPKY----EF 104

Db   52 PSECTPIHLNLVARHGTRSPTK-KRLRELESLAGRFKELVRDAEARKLPSDKIPGWLGQW 110

Db 105 LNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGG---DVPFVRAAGDQRVVDSST 161

Qy 111 KSPWEGKVKGGELIRQGEDELYQLGIRVRERFPSLFEEDYHPDVYTIRATQIPRASASAV 170

Qy 162 NWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC-PNEVDGDESTTWLGVF--APNITA 218

Db 171 AFGMG----------LFSBKGNLGPGRNRAFAVTSENRASDTKLRFFECCQNYKS 215

Qy 219 RLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVS-------YEY 268

Db 216 YRKAKEPAVDKLKEPVL--------NKITASVAKRYDLKFTKQDISSLWFLCKQVALLEW 267

Qy 269 YYDLDKYYGTGPGNALGPVQGVGVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTF 328

Db 268 TDDLEVFLLKGYGNSLNYKMGVPLLEDVLHSM------BEAIKAREEKLPPGSYEKAR-- 319

Db   :|| |. ---------GPY------YSFPGDY 54

Db   14 LVNAGTIPLGKLSDIDKIGTQTBIFPFLGGS-------GPY------YSFPGDY 54

Qy   57 -----PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVY 110

Db   55 GISRDLPESCEMKQVQMVGRHGERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLND-DY 113

Qy 111 KFGVAD-------LLPF-GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGD 153

Db 114 EFFIRDTKNLEMETTLANSVNVLNPYTGEMNAKRHARDFLAQYGMVENQTSFAVFTSNS 173

Qy 154 QRVVDSSTNWTAGFGDASGETVLPTLQVVLQEE---GNCTLCNNMCP---NEVDGDESTT 207

Db 174 NRCHDTAQYFIDGLGDKFN----ISLQTISEAESAGANTLSAHHSCPAWDDDVNDDILKK 229

Qy 208 WLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYE 267

Db 230 YDTKYLSGIAKRLNKENKGLNLTSSDANTFFAWCAYE-INARGYSDICNIFTKDELVRFS 288

Qy 268 YYYDLDKYYGTGPGNALGPVQGVGVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRT 327

Db 289 YGQDLETYYQTGPGYDVVRSVGANLFNASVKLLKESEVDQ----------------K 330

Qy 328 FYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVD---------SKLVPFSGHM 376

Db 331 VWLSFTHDTDILNYLTTIGIID--------DQNNLTAEHVPFMENTFHRSWYVPQGARV 381

Qy 377 TVEKLACSGKEAVRLVNDAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG-DFAK 432

Db 382 YTEKFQCSNDTYRYVRYVINDAVVPIETCSTGPGFSCEINDFYD---YAEKRVAGTDFLK 436

RESULT 14
S48996
acid phosphatase (EC 3.1.3.2) PHO12 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR215w
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48996; S59659
R;Macri, C.
A;Description: The sequence of S. cerevisiae cosmid 9177.
submitted to the EMBL Data Library, February 1994
A;Reference number: S46671
A;Accession: S48996
A;Molecule type: DNA
A;Residues: 1-467 <MAC>
A;Cross-references: UNIPROT:P38693; EMBL:U00029; NID:g551322; PIDN:AAB69729.1; PID:g4589
R;Xu, L.
submitted to the EMBL Data Library, January 1995
A;Reference number: S59658
A;Accession: S59659
A;Molecule type: DNA
A;Residues: 1-16,'L',18-81,'AR',84-149,'H',151-467 <XUL>
A;Cross-references: EMBL:U19789; NID:g847754; PIDN:AAA73479.1; PID:g847755
C;Genetics:
A;Gene: SGD:PHO12
A;Cross-references: SGD:S0001258; MIPS:YHR215w
A;Map position: 8R
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase

Query Match   13.4%;   Score 312.5;   DB 2;   Length 467;
Best Local Similarity   24.1%;   Pred. No. 1.8e-17;
Matches 115;   Conservative 66;   Mismatches 196;   Indels 101;   Gaps   17;

Qy   1 MVSSAFAPSILLSLMSSLALSTQ-FSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAP-- 56

Db   14 LVNAGTIPLGKLSDIDKIGTQTBIFPFLGGS-------GPY------YSFPGDY 54

Qy   57 -----PEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVY 110

Db   55 GISRDLPESCEMKQVQMVGRHGERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLND-DY 113

Qy 111 KFGVAD-------LLPF-GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGD 153

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Qy   329 YADFSHDNTMVPIFAALGLFNATALD-----------------PLKPDENRLWVDSKLVPFS 373
             |:||   |::||     ||||        |      |    |:|:  |  |  |  ||
Db   320 -LRFAHAETIVPFSCLLGLP----LDGSEFEKIQKEKPLELPPQPPKTRDFRGSTMAPFG 374

Qy   374 GHMTVEKLAC-----SGKEAVRVLVNDAVQPLEFCGGVDGVCELSAF 415
             |: :.:|  |      ||||:  |:||:     ||:|     ||
Db   375 GNNILVLYSCPAESSPKYFVQVLHNEHPIAVPGCDGKD-FCPLEDF 419
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Search completed: May 27, 2005, 08:34:48
Job time : 43 secs

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              GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        May 27, 2005, 08:33:17 ; Search time 142 Seconds
                                         (without alignments)
                                         1066.499 Million cell updates/sec

Title:         US-10-734-510-7
Perfect score: 2325
Sequence:      1 MVSSAFAPSILLSLMSSLAL.........TYARENGQGDFAKCGFVPSE 439

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      142099 seqs, 34497247 residues

Total number of hits satisfying chosen parameters:      142099

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA:*
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    2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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    8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
    9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
   10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
   11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
   12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
   13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
   14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	2325	100.0	439	10	US-09-999-214-24	Sequence 24, Appl
2	2325	100.0	439	13	US-10-083-452-7	Sequence 7, Appli
3	2325	100.0	439	16	US-10-734-510-7	Sequence 7, Appli
4	2325	100.0	439	17	US-10-732-923-11099	Sequence 11099, A
5	2254	96.9	423	15	US-10-358-960-2	Sequence 2, Appli
6	2238	96.3	419	15	US-10-442-538-122	Sequence 122, App
7	2191	94.2	409	15	US-10-442-538-145	Sequence 145, APP
8	2189	94.2	409	17	US-10-732-923-11118	Sequence 11118, A
9	1347	57.9	442	15	US-10-442-538-137	Sequence 137, App
10	1204	51.8	442	10	US-09-999-214-26	Sequence 26, Appl
11	1204	51.8	442	17	US-10-732-923-11100	Sequence 11100, A
12	1202	51.7	442	10	US-09-999-214-28	Sequence 28, Appl
13	1202	51.7	442	13	US-10-083-452-4	Sequence 4, Appli
14	1202	51.7	442	16	US-10-734-510-4	Sequence 4, Appli
15	1202	51.7	442	17	US-10-732-923-11101	Sequence 11101, A
16	1201.5	51.7	422	15	US-10-442-538-119	Sequence 119, App
17	1195.5	51.4	413	15	US-10-442-538-142	Sequence 142, App
18	1191.5	51.2	422	15	US-10-442-538-118	Sequence 118, App
19	1189.5	51.2	413	15	US-10-442-538-141	Sequence 141, App
20	1160	49.9	443	10	US-09-999-214-30	Sequence 30, Appl
21	1160	49.9	443	13	US-10-083-452-5	Sequence 5, Appli
22	1160	49.9	443	16	US-10-734-510-5	Sequence 5, Appli
23	1160	49.7	443	17	US-10-732-923-11098	Sequence 11098, A
24	1155.5	49.7	420	15	US-10-442-538-120	Sequence 120, App
25	1153	49.6	453	10	US-09-999-214-22	Sequence 22, Appl
26	1153	49.6	453	13	US-10-083-452-6	Sequence 6, Appli
27	1153	49.6	453	16	US-10-734-510-6	Sequence 6, Appli
28	1153	49.6	453	17	US-10-732-923-11145	Sequence 11145, A
29	1150	49.5	410	15	US-10-442-538-143	Sequence 143, App
30	1149	49.4	435	15	US-10-442-538-121	Sequence 121, App
31	1148	49.4	425	15	US-10-442-538-144	Sequence 144, App
32	1144.5	49.2	369	15	US-10-442-538-123	Sequence 123, App
33	941.5	40.5	467	15	US-10-442-538-169	Sequence 169, App
34	831.5	35.8	467	15	US-10-442-538-139	Sequence 139, App
35	830.5	35.7	467	15	US-10-442-538-163	Sequence 163, App
36	829	35.7	457	17	US-10-492-782-42	Sequence 42, Appl
37	824.5	35.5	433	15	US-10-492-782-5	Sequence 5, Appli
38	824.5	35.5	440	17	US-10-492-782-6	Sequence 6, Appli
39	824.5	35.5	440	17	US-10-492-782-26	Sequence 26, Appl
40	824.5	35.5	440	17	US-10-492-782-27	Sequence 27, Appl
41	823	35.4	447	17	US-10-492-782-30	Sequence 30, Appl
42	823	35.4	461	17	US-10-492-782-37	Sequence 37, Appl
43	823	35.4	466	15	US-10-442-538-113	Sequence 113, App
44	823	35.4	466	15	US-10-442-538-136	Sequence 136, App
45	823	35.4	466	15	US-10-442-538-159	Sequence 159, App

ALIGNMENTS

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RESULT 1
US-09-999-214-24
; Sequence 24, Application US/09999214
; Publication No. US2003006497A1
; GENERAL INFORMATION:
;   APPLICANT: Lassen, Soren F.
;   APPLICANT: Bech, Lisbeth
;   APPLICANT: Ohmann, Anders
;   APPLICANT: Breinholt, Jens
;   APPLICANT: Fuglsang, Claus C.
;   APPLICANT: Ostergaard, Peter R.
;   TITLE OF INVENTION: Phytase Polypeptides
;   FILE REFERENCE: 5383,500-US
;   CURRENT APPLICATION NUMBER: US/09/999,214
;   CURRENT FILING DATE: 2001-11-30
;   PRIOR APPLICATION NUMBER: 09/482,558
;   PRIOR FILING DATE: 2000-01-13
;   PRIOR APPLICATION NUMBER: 08/993,359
;   PRIOR FILING DATE: 1997-12-19
;   PRIOR APPLICATION NUMBER: 1481/96
;   PRIOR FILING DATE: 1996-12-20
;   PRIOR APPLICATION NUMBER: 0301/97
;   PRIOR FILING DATE: 1997-03-18
;   PRIOR APPLICATION NUMBER: 0529/97
;   PRIOR FILING DATE: 1997-05-07
;   PRIOR APPLICATION NUMBER: 1388/97
;   PRIOR FILING DATE: 1997-12-01
;   PRIOR APPLICATION NUMBER: 60/046,082
;   PRIOR FILING DATE: 1997-05-09
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Peniophora lycii
;   FEATURE:
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;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(30)
US-09-999-214-24
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Best Local Similarity    100.0%;   Pred. No. 1.8e-216;
Matches 439;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1  MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC  60

Qy     61  TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF  120
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Qy    121  GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ  180
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Qy    181  VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM  240
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Db    241  CPFDTLSSGNASPFCDLFTAEEVYSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL  300

Qy    301  TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE  360
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Db    301  TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE  360

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RESULT 2
US-10-083-452-7
;   Sequence 7, Application US/10083452
;   Publication No. US2002127218A1
;   GENERAL INFORMATION:
;   APPLICANT: Svendsen, Allan
;   TITLE OF INVENTION: Phytase Variants
;   FILE REFERENCE: 5618.500-US
;   CURRENT APPLICATION NUMBER: US/10/083,452
;   CURRENT FILING DATE:  2002-02-26
;   PRIOR APPLICATION NUMBER: US/09/273,871
;   PRIOR FILING DATE: 1999-03-22
;   PRIOR APPLICATION NUMBER: PA 1998 00407
;   PRIOR FILING DATE: 1998-03-23
;   PRIOR APPLICATION NUMBER: PA 1998 00806
;   PRIOR FILING DATE: 1998-06-19
;   PRIOR APPLICATION NUMBER: PA 1998 01176
;   PRIOR FILING DATE: 1998-09-18
;   PRIOR APPLICATION NUMBER: PA 1999 00091
;   PRIOR FILING DATE: 1999-01-22
;   PRIOR APPLICATION NUMBER: 60/080,129
;   PRIOR FILING DATE: 1998-03-31
;   PRIOR APPLICATION NUMBER: 60/090,675
;   PRIOR FILING DATE: 1998-06-25
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Peniophora ycii
US-10-083-452-7
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Query Match              100.0%;   Score 2325;  DB 13;  Length 439;
Best Local Similarity    100.0%;   Pred. No. 1.8e-216;
Matches 439;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1  MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC  60

Qy     61  TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF  120
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Qy    121  GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ  180
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Qy    181  VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM  240
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Db    181  VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM  240

Qy    241  CPFDTLSSGNASPFCDLFTAEEVYSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL  300
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Db    241  CPFDTLSSGNASPFCDLFTAEEVYSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL  300

Qy    301  TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE  360
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Db    301  TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE  360

Qy    361  NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT  420
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Db    361  NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT  420

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RESULT 3
US-10-734-510-7
;   Sequence 7, Application US/10734510
;   Publication No. US2004017S376A1
;   GENERAL INFORMATION:
;   APPLICANT: Svendsen, Allan
;   TITLE OF INVENTION: Phytase Variants
;   FILE REFERENCE: 5618.500-US
;   CURRENT APPLICATION NUMBER: US/10/734,510
;   CURRENT FILING DATE:  2003-12-12
;   PRIOR APPLICATION NUMBER: US/09/273,871A
;   PRIOR FILING DATE: 1999-03-22
;   PRIOR APPLICATION NUMBER: PA 1998 00407
;   PRIOR FILING DATE: 1998-03-23
;   PRIOR APPLICATION NUMBER: PA 1998 00806
;   PRIOR FILING DATE: 1998-06-19
;   PRIOR APPLICATION NUMBER: PA 1998 01176
;   PRIOR FILING DATE: 1998-09-18
;   PRIOR APPLICATION NUMBER: PA 1999 00091
;   PRIOR FILING DATE: 1999-01-22
;   PRIOR APPLICATION NUMBER: 60/080,129
;   PRIOR FILING DATE: 1998-03-31
;   PRIOR APPLICATION NUMBER: 60/090,675
;   PRIOR FILING DATE: 1998-06-25
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Peniophora ycii
US-10-734-510-7
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Query Match              100.0%;   Score 2325;  DB 16;  Length 439;
Best Local Similarity    100.0%;   Pred. No. 1.8e-216;
Matches 439;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy   61  TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
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Db   61  TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy  121  GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
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Db  121  GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy  181  VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
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Db  181  VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy  241  CPFDTLSSGNASPFCDLFTAEEVVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
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RESULT 4
US-10-732-923-11099
; Sequence 11099, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
;   APPLICANT: Edgerton, Michael D
;   TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;   FILE REFERENCE: 38-15(52796)C
;   CURRENT APPLICATION NUMBER: US/10/732,923
;   CURRENT FILING DATE: 2003-12-10
;   PRIOR APPLICATION NUMBER: 10/310,154
;   PRIOR FILING DATE: 2002-12-04
;   NUMBER OF SEQ ID NOS: 24149
;   SEQ ID NO 11099
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Peniophora lycii
US-10-732-923-11099

  Query Match   100.0%; Score 2325; DB 17; Length 439;
  Best Local Similarity   100.0%; Pred. No. 1.8e-216;
  Matches 439; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1  MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC  60
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Db    1  MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC  60

Qy   61  TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
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Db  121  GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy  181  VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
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Qy  301  TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
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Db  301  TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy  361  NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
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Db  361  NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy  421  YARENGQGDFAKCGFVPSE 439
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Db  421  YARENGQGDFAKCGFVPSE 439
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RESULT 5
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; Sequence 2, Application US/10358960
; Publication No. US20030208788A1
; GENERAL INFORMATION:
;   APPLICANT: Matsui, Tomoko
;   APPLICANT: Fuglsang, Claus
;   APPLICANT: Svendsen, Allan
;   APPLICANT: Fukuyama, Shiro
;   TITLE OF INVENTION: Phytase Variants
;   FILE REFERENCE: 10261.200-US
;   CURRENT APPLICATION NUMBER: US/10/358,960
;   CURRENT FILING DATE: 2003-02-05
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 2
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Peniophora lycii
US-10-358-960-2

  Query Match   96.9%; Score 2254; DB 15; Length 423;
  Best Local Similarity 100.0%; Pred. No. 1.3e-209;
  Matches 423; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   17  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  76
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Db    1  SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWP  60

Qy   77  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 136
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Db   61  TSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 120

Qy  137  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 196
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Db  121  STLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMC 180

Qy  197  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 256
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Db  181  PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCD 240

Qy  257  LFTAEEVVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 316
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Db  241  LFTAEEVVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLD 300

Qy  317  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
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Db  301  SDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

Qy  377  TVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
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Qy  437  PSE 439
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Db  421  PSE 423
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RESULT 6
US-10-442-538-122
; Sequence 122, Application US/10442538
; Publication No. US20030224491A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/10/442,538
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 419
; TYPE: PRT
; ORGANISM: P. lycii
US-10-442-538-122

Query Match   96.3%; Score 2238; DB 15; Length 419;
Best Local Similarity 100.0%; Pred. No. 4.5e-208;
Matches 419; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   21 STQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 STQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA 60

Qy   81 RSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLF 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLF 120

Qy   141 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV 180

Qy   201 DGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTA 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 DGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTA 240

Qy   261 EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPA 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPA 300

Qy   321 TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 360

Qy   381 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 419

RESULT 7
US-10-442-538-145
; Sequence 145, Application US/10442538
; Publication No. US20030224491A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/10/442,538
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 409
; TYPE: PRT
; ORGANISM: P. lycii
US-10-442-538-145

Query Match   94.2%; Score 2191; DB 15; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 409; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 LPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK 60

Qy   91 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 120

Qy   151 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGDESTTWLG 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGDESTTWLG 180

Qy   211 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYY 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTAEEYVSYEYYY 240

Qy   271 DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 300

Qy   331 DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 360

Qy   391 VLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 409

RESULT 8
US-10-732-923-11118
; Sequence 11118, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11118
; LENGTH: 409
; TYPE: PRT
; ORGANISM: synthetic construct
US-10-732-923-11118

Query Match   94.2%; Score 2189; DB 17; Length 409;
Best Local Similarity   99.8%; Pred. No. 2.5e-203;
Matches 408; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK 90
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK 60

Qy   91 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 120

```
Qy   151 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEGNCTLCNNMCPNEVDGDESTTWLG 210
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEGNCTLCNNMCPNEVDGDESTTWLG 180

Qy   211 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTABEEVVSYEYYY 270
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTABEEVVSYEYYY 240

Qy   271 DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 330
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 300

Qy   331 DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 390
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 360

Qy   391 VLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 409
```

RESULT 9
US-10-442-538-137
; Sequence 137, Application US/10442538
; Publication No. US20030224491A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C3845/111692
; CURRENT APPLICATION NUMBER: US/10/442,538
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Basidio
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: n is unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: x is unknown
US-10-442-538-137

```
Query Match      57.9%;  Score 1347;  DB 15;  Length 442;
Best Local Similarity   61.8%;  Pred. No. 1.4e-121;
Matches 267;  Conservative 32;  Mismatches 32;  Indels 111;  Gaps 5;

Qy    28 AAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAA 87
            |||||||:|:  | :|||:|:|:|||:||:|| |:| ||:||||||:||||||:|:||||
Db     9 AAQLPIPXQKQXXWSPYSPYFPVAXYXAPPAGCQIXQXVNIIQRHGARFPTSGAATRIQAA 68

Qy    88 VAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPF 147
            ||| |   |||| | ||| | || |: ||:|||||:|| | |:| |||| :| :  :|||
Db    69 VAKLQSAXXXTDPKLDFLKNXTYXLGXDDLVPFGAXQSSQAGQEAFTRYSXLVSXDNLPF 128

Qy   148 VRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEGNCTLCNNMCPNEVDGD-EST 206
            ||| | |||||: ||||||  :| ::||  :| ::|  || ||:::||| : :|| :
Db   129 VRASGSDRVVDSAATNWTAGFAXAXSXNTXXPXLXVILSEXGNDTLDDNMCPXAGDSDPQXN 188

Qy   207 TWLGVFAPNITARLNAAAPGANLTPXDAXNLXXLCPFETVSXEXXSXFCDLFEXXPEEFX 264
            :||:||||:||||||||||||||| :||:||||||||||||:||||||||||||||||||
Db   189 XWLAVFAPPITARLNAAAPGANLTDXDAXNLXXLCPFETVSXEXXSXFCDLFEXXPEEFX 248
```

```
Qy   265 SYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPL 324
            :: |  ||||:|||| |  |||||||||:|||||||:|||||:||||||||||:|:||||
Db   249 AFXYXGDLDKFYGTGYGQPLGPVQGVGYINELLARLTXQAVRDNTQTNRTLDSSPXTFPL 308

Qy   325 NRTFYADFSHDNTMVPIFAALGLFNATA-LDPLKPDENRLWVDSKLVPFSGHMTVEKLAC 383
            ||||||||||||: |  || ::|||| | |||  |||| ||:||||||||  |:||||:|
Db   309 NRTFYADFSHDNQMVAIFSAMGLFNQSAPLDPSXPDNRTWVTSKLVPFSARMVVERLXC 368

Qy   384 ----------------SGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFVESQTYAREN 425
                            :   :|||||||||||||||||| :||:|  :|||||:||||:
Db   369 XXXGTXXXXXXXXXXXXXXXVRVLVNDAVQPLEFCGGDXGXCTLDAFVESQXYARED 428

Qy   426 GQGDFAKCGFVP 437
            ||||| ||  :|
Db   429 GQGDFEKCFATP 440
```

RESULT 10
US-09-999-214-26
; Sequence 26, Application US/09999214
; Publication No. US20030064497A1
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/999,214
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/482,558
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 08/993,359
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 1481/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involutus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-999-214-26

```
Query Match      51.8%;  Score 1204;  DB 10;  Length 442;
Best Local Similarity   55.3%;  Pred. No. 1.1e-107;
Matches 242;  Conservative 51;  Mismatches 139;  Indels 6;  Gaps 5;

Qy     1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
           |:  ::| ||:||:| |:| |: ::    ||||| |:|:| :||  :|:|:|  |||:||
Db     1 MLFGFVALACLLSLSBVLATSVPKN-TAPTFPIPESEQRNWSPYSYFPLABYKAPPAGC 59

Qy    61 TVTQVNLIQRHGARWPTSGARSRQVAVAKIQMARPFTDPKYEFLNDFVYKFPGVADLLPF 120
           :: ||:|||||||:||||| : : :   | ::     |||| |:| : |:   :|:|||
Db    60 QINQVNIIQRHGARFPTSGATTRIKAGLTKLQGVQNFTDAKFNFIKSFKYDLGNSDLVPF 119

Qy   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
           ||:||  | |:| |||| :| :  :|| ||: | |||||: ||||||  :|  :::|  :
Db   120 GAAQSPDAGQBAFARYSKLVSKNNLPFIRADGSDRVVDSATNWTAGFASASHNTVQPKLN 179
```

Qy 181 VVLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMD 239
Db 180 LILPQTGNDTLEDNMCPAAGDSDPQVNAWLAVAFPSITARLNAAAPSVNLTDTDAFNLVS 239

Qy 240 MCPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELL 297
Db 240 LCAFLTVSKEKKSDFCTLFEGIPGSFEAFAYGGDLDKFYGTGYGQELGPVQGVGYVNELi 299

Qy 298 ARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPL 356
Db 300 ARLTNSAVRDNTQTNRTLDDASPVTFPLNKTFYADFSHDNLMVAVFSAMGLFRQPAPLSTS 359

Qy 357 KPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAF 415
Db 360 VPNPWRTWRTSSLVPFSGRMVVERLSCFGTTKVRVLVQDQVQPLEFCCGDRNGLCTLAKF 419

Qy 416 VESQTYARENGQGDFAKC 433
Db 420 VESQTFARSDGAGDFEKC 437

RESULT 11
US-10-732-923-11100
; Sequence 11100, Application US/10732923
; Publication No. US2005010879A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11100
; LENGTH: 442
; TYPE: PRT
; ORGANISM: cf. Ceriporia sp. CBS 100231
US-10-732-923-11100

Query Match   51.8%; Score 1204; DB 17; Length 442;
Best Local Similarity   55.3%; Pred. No. 1.1e-107;
Matches 242; Conservative   51; Mismatches 139; Indels   6; Gaps   5;

Qy   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
Db   1 MLFGFVALACLLSLSEVLATSVPKN-TAPTFPIPESEQRNWSPYSPYFPLAEYKAPPAGC 59

Qy   61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
Db   60 QINQVNIIQRHGARFPPTSGATTRIKAGLTKLQGVQNFTDAKFNFIKSFKYDLGNSDLVPF 119

Qy 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
Db 120 GAAQSFDAGQEAFARYSKLVSKNNLPFIRADGSDRVVDSATNWTAGFASASHNTVQPKLN 179

Qy 181 VVLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMD 239
Db 180 LILPQTGNDTLEDNMCPAAGDSDPQVNAWLAVAFPSITARLNAAAPSVNLTDTDAFNLVS 239

Qy 240 MCPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELL 297
Db 240 LCAFLTVSKEKKSDFCTLFEGIPGSFEAFAYGGDLDKFYGTGYGQELGPVQGVGYVNELi 299

Qy 298 ARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPL 356
Db 300 ARLTNSAVRDNTQTNRTLDDASPVTFPLNKTFYADFSHDNLMVAVFSAMGLFRQPAPLSTS 359

Qy 357 KPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAF 415
Db 360 VPNPWRTWRTSSLVPFSGRMVVERLSCFGTTKVRVLVQDQVQPLEFCCGDRNGLCTLAKF 419

Qy 416 VESQTYARENGQGDFAKC 433
Db 420 VESQTFARSDGAGDFEKC 437

RESULT 12
US-09-999-214-28
; Sequence 28, Application US/09999214
; Publication No. US2003064497A1
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/999,214
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/482,558
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 08/993,359
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 1481/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involtus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-999-214-28

Query Match   51.7%; Score 1202; DB 10; Length 442;
Best Local Similarity   52.6%; Pred. No. 1.7e-107;
Matches 230; Conservative   61; Mismatches 128; Indels   18; Gaps   5;

Qy   2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT 61
Db   14 LSEVFAASVPRN------------IAPKFPIPESEQRNWSPYSPYFPLAEYKAPPAGCE 60

Qy   62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
Db   61 INQVNIIQRHGARFPPTSGATTRIKAGLSKLQSVQNFTDPKFDFIKSFTYDLGTSDLVPFG 120

Qy 122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
Db 121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL 180

Qy 182 VLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
Db 181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFPSVTAQLNAAAPGANLTDADAFNLVSL 240

Qy 241 CPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYGTGPGNALGPVQGVGYVNELLA 298
Db 241 CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTGYGQALGPVQGVGYINELLA 300

Qy 299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
Db 301 RLTNSAVNDNTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360

Qy 358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV 416

Left column (RESULT 13)

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Db   361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRLVQDQVQPLEFCGGDQDGLCALDKFV 420
             ||||: :|||||  |||: :||||  |||||||||||||
Qy   417 ESQTYARENGQGDFAKC 433
             |||  ||| |||:|||
Db   421 ESQAYARSGGAGDFEKC 437
```

RESULT 13
US-10-083-452-4
; Sequence 4, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involtus
US-10-083-452-4

Query Match   51.7%;   Score 1202; DB 13; Length 442;
Best Local Similarity 52.6%;   Pred. No. 1.7e-107;
Matches 230; Conservative   61; Mismatches 128; Indels 18; Gaps   5;

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Qy     2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT 61
           :|: |||: :                  |||: |  :|:|||   |  ||||
Db    14 LSEVFAASVPRN----------IAPKFSIPESEQRNWSPYSPYFPLAEYKAPPAGGE 60

Qy    62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
           :|||||||||: ::||||| :|||||:|:|||:    ||:||::|:|||||:|
Db    61 INQVNIIQRHGARFPTSGAATRIKAGLSKLQSVQNFTDPKFDFIKSFTYDLGTSDLVPFG 120

Qy   122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
           |:||  |||:  | ::||||:||||:|:: |||||||||:||||||  |||  ||||
Db   121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL 180

Qy   182 VLQEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
           :|: ||||| |: |||:  |  : ::||||:|||: ||||: |::||||
Db   181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFPSVTAQLNAAARPGANLTDADAFNLVSL 240

Qy   241 CPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLA 298
           ||| :|::  |: :||:| |     :::|| ::| |||:|||  ||||||||:|||||:
Db   241 CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLLKFYGTGYGQALGPVQGVGYINELLA 300

Qy   299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
           |||  ||:|:|:||||:|:|  |||||::|||||||||||||||: :|:|||  |||:
Db   301 RLTNSAVNDNTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360

Qy   358 PDENRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV 416
           ||:|| | :|::: || ::|  ||  :: :||||: :|:|||||| ||   ||| : |||
Db   361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRLVQDQVQPLEFCGGDQDGLCALDKFV 420

Qy   417 ESQTYARENGQGDFAKC 433
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Right column (RESULT 14)

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Db   421 ESQAYARSGGAGDFEKC 437
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RESULT 14
US-10-734-510-4
; Sequence 4, Application US/10734510
; Publication No. US2004017576A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/734,510
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/09/273,871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involtus
US-10-734-510-4

Query Match   51.7%;   Score 1202; DB 16; Length 442;
Best Local Similarity 52.6%;   Pred. No. 1.7e-107;
Matches 230; Conservative   61; Mismatches 128; Indels 18; Gaps   5;

```
Qy     2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT 61
           :|: |||: :                  |||: |  :|:|||   |  ||||
Db    14 LSEVFAASVPRN----------IAPKFSIPESEQRNWSPYSPYFPLAEYKAPPAGGE 60

Qy    62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
           :|||||||||: ::||||| :|||||:|:|||:    ||:||::|:|||||:|
Db    61 INQVNIIQRHGARFPTSGAATRIKAGLSKLQSVQNFTDPKFDFIKSFTYDLGTSDLVPFG 120

Qy   122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
           |:||  |||:  | ::||||:||||:|:: |||||||||:||||||  |||  ||||
Db   121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL 180

Qy   182 VLQEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
           :|: ||||| |: |||:  |  : ::||||:|||: ||||: |::||||
Db   181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFPSVTAQLNAAAPDGANLTDADAFNLVSL 240

Qy   241 CPFDTLSSGNASPFCDLFTA--EEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLA 298
           ||| :|::  |: :||:| |     :::|| ::| |||:|||  ||||||||:|||||:
Db   241 CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLLKFYGTGYGQALGPVQGVGYINELLA 300

Qy   299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
           |||  ||:|:|:||||:|:|  |||||::|||||||||||||||: :|:|||  |||:
Db   301 RLTNSAVNDNTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360

Qy   358 PDENRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV 416
           ||:|| | :|::: || ::|  ||  :: :||||: :|:|||||| ||   ||| : |||
Db   361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRLVQDQVQPLEFCGGDQDGLCALDKFV 420

Qy   417 ESQTYARENGQGDFAKC 433
           |||  ||| |||:|||
Db   421 ESQAYARSGGAGDFEKC 437
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RESULT 15
US-10-732-923-11101
; Sequence 11101, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
;   APPLICANT: Edgerton, Michael D
;   TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;   FILE REFERENCE: 38-15(52796)C
;   CURRENT APPLICATION NUMBER: US/10/732,923
;   CURRENT FILING DATE: 2003-12-10
;   PRIOR APPLICATION NUMBER: 10/310,154
;   PRIOR FILING DATE: 2002-12-04
;   NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11101
;   LENGTH: 442
;   TYPE: PRT
;   ORGANISM: cf. Ceriporia sp. CBS 100231
US-10-732-923-11101

Query Match   51.7%;   Score 1202; DB 17;   Length 442;
Best Local Similarity 52.6%;   Pred. No. 1.7e-107;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps 5;

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Qy     2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT  61
           :|  |:    :   :           :| :   |  | |||| |||
Db    14 LSEVFAASVPRN----------IAPKFSIPESEQRNWSPYSPYFPLAEYKAPPAGCE   60

Qy    62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
          :|||:|||||||||::| :| |    :  :  |||||::|  |  |  |:||:||||||
Db    61 INQVNIIQRHGARFPTSGAATRIKAGLSKLQSVQNFTDPKFDFIKSFTYDLGTSDLVPFG 120

Qy   122 ANQSHQTGTDMYTRYSTLPEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
          |  | |  ||||:  || |   |  ||  : :|||||: |: |||| :| |  | |  :
Db   121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL 180

Qy   182 VLQEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          :| :    ||   :|||    : |||  | |   |   ||::|||:: |:   :
Db   181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFPSVTAQLNAAAPGANLTDADAFNLVSL 240

Qy   241 CPFDTLSSGNASPFCDLFTA--EBYVSYEYYYDLDKYYGTGPGNALGPVQGYVNELLA 298
          |||:|:||||:||||:||     :: || |:|||:||||:|||:|||||:||||:||
Db   241 CPFMTVSXEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTGYGQALGPVQGVYINELLA 300

Qy   299 RLTGQAVRDETQTNRTLDSDPATPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
          |||:|| |||||:||||:| ||:|||||||||||||||||||:|:||:|:||| |||||
Db   301 RLTNSAVNDNTQTNRTLDAAPDFTPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360

Qy   358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV 416
          ||:|| ||::|:||||| ||:||  | | | |  |:|:|||| |  ||   |:|| | |
Db   361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRVLVQDQVQPLEFCGGDQDDGLCALDKFV 420

Qy   417 ESQTYARENGQGDFAKC 433
          ||| |||| |:||| ||
Db   421 ESQAYARSGAGDFEKC 437
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Search completed: May 27, 2005, 08:46:20
Job time : 144 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:     May 27, 2005, 08:27:27 ; Search time 43 Seconds
                              (without alignments)
                              762.115 Million cell updates/sec

Title:         US-10-734-510-7
Perfect score: 2325
Sequence:      1 MVSSAFAPSILLSLMSSLAL.........TYARENGQDFAKCGFVPSE 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:      513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:      513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
             1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
             2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
             3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
             4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
             5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
             6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match Match	Length	DB	ID	Description
1	2325	100.0	439	3	US-08-993-359-24	Sequence 24, Appl
2	2325	100.0	439	3	US-09-221-654-2	Sequence 2, Appli
3	2325	100.0	439	3	US-08-989-358A-2	Sequence 2, Appli
4	2325	100.0	439	4	US-09-273-871A-7	Sequence 7, Appli
5	2325	100.0	439	4	US-09-482-558A-24	Sequence 24, Appl
6	2325	100.0	439	4	US-10-083-452-7	Sequence 7, Appli
7	2238	96.3	439	4	US-09-684-855-122	Sequence 122, App
8	2238	96.3	419	4	US-09-488-265B-21	Sequence 21, Appl
9	2191	94.2	409	4	US-09-684-855-145	Sequence 145, App
10	1347	57.9	442	3	US-09-684-855-137	Sequence 137, App
11	1204	51.8	442	4	US-08-993-359-26	Sequence 26, Appl
12	1204	51.8	442	4	US-09-482-558A-26	Sequence 26, Appl
13	1202	51.7	442	3	US-08-993-359-28	Sequence 28, Appl
14	1202	51.7	442	4	US-09-273-871A-4	Sequence 4, Appli
15	1202	51.7	442	4	US-09-482-558A-28	Sequence 28, Appl
16	1202	51.7	442	4	US-10-083-452-4	Sequence 4, Appli
17	1201.5	51.7	422	4	US-09-684-855-119	Sequence 119, Appli
18	1201.5	51.7	422	4	US-09-488-265B-18	Sequence 18, Appl
19	1195.5	51.4	413	4	US-09-684-855-142	Sequence 142, App
20	1191.5	51.2	422	4	US-09-684-855-118	Sequence 118, App
21	1191.5	51.2	422	4	US-09-488-265B-17	Sequence 17, Appl
22	1189.5	51.2	413	4	US-09-684-855-141	Sequence 141, App
23	1160	49.9	443	3	US-08-993-359-30	Sequence 30, Appl
24	1160	49.9	443	4	US-09-273-871A-5	Sequence 5, Appli
25	1160	49.9	443	4	US-09-482-558A-30	Sequence 30, Appl
26	1160	49.9	443	4	US-10-083-452-5	Sequence 5, Appli
27	1155.5	49.7	420	4	US-09-684-855-120	Sequence 120, App
28	1155.5	49.7	420	4	US-09-488-265B-19	Sequence 19, Appl
29	1153	49.6	453	3	US-08-993-359-22	Sequence 22, Appl
30	1153	49.6	453	4	US-09-273-871A-6	Sequence 6, Appli
31	1153	49.6	453	4	US-09-482-558A-22	Sequence 22, Appl
32	1153	49.6	453	4	US-10-083-452-6	Sequence 6, Appli
33	1150	49.5	410	4	US-09-684-855-143	Sequence 143, App
34	1149	49.4	435	4	US-09-684-855-121	Sequence 121, App
35	1149	49.4	435	4	US-09-488-265B-20	Sequence 20, App
36	1148	49.4	425	4	US-09-684-855-144	Sequence 144, App
37	1144.5	49.2	369	4	US-09-684-855-123	Sequence 123, App
38	1144.5	49.2	369	4	US-09-488-265B-22	Sequence 22, Appl
39	941.5	40.5	467	4	US-09-684-855-169	Sequence 169, App
40	941.5	40.5	467	4	US-09-488-265B-36	Sequence 36, Appl
41	831.5	35.8	441	4	US-09-488-265B-24	Sequence 24, Appl
42	831.5	35.8	467	4	US-09-684-855-139	Sequence 139, App
43	831.5	35.8	467	4	US-09-488-265B-26	Sequence 26, Appl
44	830.5	35.7	467	4	US-09-684-855-163	Sequence 163, App
45	830.5	35.7	467	4	US-09-488-265B-31	Sequence 31, Appl

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                              ALIGNMENTS

RESULT 1
US-08-993-359-24
;  Sequence 24, Application US/08993359A
;  Patent No. 6039942
;  GENERAL INFORMATION:
;  APPLICANT: Lassen, Soren F.
;  APPLICANT: Bech, Lisbeth
;  APPLICANT: Ohmann, Anders
;  APPLICANT: Breinholt, Jens
;  APPLICANT: Fuglsang, Claus C.
;  APPLICANT: Ostergaard, Peter R.
;  TITLE OF INVENTION: Phytase Polypeptides
;  FILE REFERENCE: 5383.500-US
;  CURRENT APPLICATION NUMBER: US/08/993,359A
;  CURRENT FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 1480/96
;  EARLIER FILING DATE: 1996-12-20
;  EARLIER APPLICATION NUMBER: 1481/96
;  EARLIER FILING DATE: 1996-12-20
;  EARLIER APPLICATION NUMBER: 0301/97
;  EARLIER FILING DATE: 1997-03-18
;  EARLIER APPLICATION NUMBER: 0529/97
;  EARLIER FILING DATE: 1997-05-07
;  EARLIER APPLICATION NUMBER: 1388/97
;  EARLIER FILING DATE: 1997-12-01
;  EARLIER APPLICATION NUMBER: 60/046,082
;  EARLIER FILING DATE: 1997-05-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
;  LENGTH: 439
;  TYPE: PRT
;  ORGANISM: Peniophora lycii
;  FEATURE:
;  NAME/KEY: SIGNAL
;  LOCATION: (1)...(30)
US-08-993-359-24

       Query Match             100.0%;  Score 2325;  DB 3;  Length 439;
       Best Local Similarity   100.0%;  Pred. No. 2.7e-250;
       Matches  439;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy         61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
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Qy  121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy  181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy  241 CPFDTLSSGNASPFCDLFTABEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CPFDTLSSGNASPFCDLFTABEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy  301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy  361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy  421 YARENGQGDFAKCGFVPSE 439
            |||||||||||||||||||
Db  421 YARENGQGDFAKCGFVPSE 439
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RESULT 2
US-09-221-654-2
; Sequence 2, Application US/09221654
; Patent No. 6054306
GENERAL INFORMATION:
APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6054306o No. 6054306disk of No. 6054306th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
FILING DATE: 12-DEC-1997
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-221-654-2

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Query Match           100.0%;  Score 2325;  DB 3;  Length 439;
Best Local Similarity 100.0%;  Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy  61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy 181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy 241 CPFDTLSSGNASPFCDLFTABEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CPFDTLSSGNASPFCDLFTABEYVSYEYYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy 301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy 361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy 421 YARENGQGDFAKCGFVPSE 439
            |||||||||||||||||||
Db 421 YARENGQGDFAKCGFVPSE 439
```

RESULT 3
US-08-989-358A-2
; Sequence 2, Application US/08989358A
; Patent No. 6060298
GENERAL INFORMATION:
APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6060298o No. 6060298disk of No. 6060298th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,358A
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1481/96

FILING DATE: 20-DEC-1996
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-358A-2

Query Match 100.0%; Score 2325; DB 3; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy 61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy 181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy 241 CPFDTLSSGNASPFCDLFTABEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CPFDTLSSGNASPFCDLFTABEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy 301 TGQAVRDETQTNRTLDSDDPATPFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 TGQAVRDETQTNRTLDSDDPATPFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy 361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy 421 YARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||
Db 421 YARENGQGDFAKCGFVPSE 439

RESULT 4
US-09-273-871A-7
; Sequence 7, Application US/09273871A
; Patent No. 651495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora ycii
US-09-273-871A-7

Query Match 100.0%; Score 2325; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60

Qy 61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy 181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy 241 CPFDTLSSGNASPFCDLFTABEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CPFDTLSSGNASPFCDLFTABEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLARL 300

Qy 301 TGQAVRDETQTNRTLDSDDPATPFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 TGQAVRDETQTNRTLDSDDPATPFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy 361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy 421 YARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||
Db 421 YARENGQGDFAKCGFVPSE 439

RESULT 5
US-09-482-558A-24
; Sequence 24, Application US/09482558A
; Patent No. 6569659
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/482,558A
; CURRENT FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: US/08/993,359
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 1480/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 1481/96

; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora lycii
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
US-09-482-558A-24

Query Match   100.0%;   Score 2325;   DB 4;   Length 439;
Best Local Similarity   100.0%;   Pred. No. 2.7e-250;
Matches 439;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1   MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC   60

Qy   61   TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy 121   GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121   GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy 181   VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181   VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy 241   CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGYVNELLARL   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241   CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGYVNELLARL   300

Qy 301   TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301   TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy 361   NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361   NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy 421   YARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||
Db 421   YARENGQGDFAKCGFVPSE 439

RESULT 6
US-10-083-452-7
; Sequence 7, Application US/10083452
; Patent No. 6689358
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora ycii
US-10-083-452-7

Query Match   100.0%;   Score 2325;   DB 4;   Length 439;
Best Local Similarity   100.0%;   Pred. No. 2.7e-250;
Matches 439;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1   MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC   60

Qy   61   TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120

Qy 121   GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121   GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180

Qy 181   VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181   VVLQEEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240

Qy 241   CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGYVNELLARL   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241   CPFDTLSSGNASPFCDLFTAEEYVSYEYYYDLDKYYGTGPGNALGPVQGYVNELLARL   300

Qy 301   TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301   TGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDE 360

Qy 361   NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361   NRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQT 420

Qy 421   YARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||
Db 421   YARENGQGDFAKCGFVPSE 439

RESULT 7
US-09-684-855-122
; Sequence 122, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 419
; TYPE: PRT
; ORGANISM: P. lycii

US-09-684-855-122

Query Match   96.3%;   Score 2238; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.3e-240;
Matches 419; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   21 STQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA   80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 STQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA   60

Qy   81 RSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLF 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLF 120

Qy   141 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV 180

Qy   201 DGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTA 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 DGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTA 240

Qy   261 EEVYSYEYYYDLDKYYGTGPGNALGPVQGVGVYVNELLARLTGQAVRDETQTNRTLDSDPA 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EEVYSYEYYYDLDKYYGTGPGNALGPVQGVGVYVNELLARLTGQAVRDETQTNRTLDSDPA 300

Qy   321 TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 360

Qy   381 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 419

RESULT 8
US-09-488-265B-21
; Sequence 21, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; APPLICANT: Lassen, Soren F
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Peniophora lycii
US-09-488-265B-21

Query Match   96.3%;   Score 2238; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.3e-240;
Matches 419; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   21 STQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA   80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 STQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGA   60

Qy   81 RSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLF 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLF 120

Qy   141 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEV 180

Qy   201 DGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTA 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 DGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTA 240

Qy   261 EEVYSYEYYYDLDKYYGTGPGNALGPVQGVGVYVNELLARLTGQAVRDETQTNRTLDSDPA 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EEVYSYEYYYDLDKYYGTGPGNALGPVQGVGVYVNELLARLTGQAVRDETQTNRTLDSDPA 300

Qy   321 TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TFPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEK 360

Qy   381 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 LACSGKEAVRVLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 419

RESULT 9
US-09-684-855-145
; Sequence 145, Application US/0968485S
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 409
; TYPE: PRT
; ORGANISM: P. lycii
US-09-684-855-145

Query Match   94.2%;   Score 2191; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 2.2e-235;
Matches 409; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK   90
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 LPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAAVAK   60

Qy   91 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 150
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPFVRA 120

Qy   151 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGDESTTWLG 210
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLQEEGNCTLCNNMCPNEVDGDESTTWLG 180

Qy   211 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTABEEVSYEYYY 270
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VFAPNITARLNAAAPSANLSDSDALTLMDMCPFDTLSSGNASPFCDLFTABEEVSYEYYY 240

Qy   271 DLDKYYGTGPGNALGPVQGVGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 330
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DLDKYYGTGPGNALGPVQGVGVGYVNELLARLTGQAVRDETQTNRTLDSDPATFPLNRTFYA 300

Qy   331 DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 390
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DFSHDNTMVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVR 360

Qy   391 VLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 439
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VLVNDAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFVPSE 409

RESULT 10
US-09-684-855-137
; Sequence 137, Application US/0968485S
; Patent No. 6599735

; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Basidio
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: n is unknown
; NAME/KEY: UNSURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: x is unknown
US-09-684-855-137

Query Match   57.9%;   Score 1347; DB 4; Length 442;
Best Local Similarity 61.8%; Pred. No. 4e-141;
Matches 267; Conservative 32; Mismatches 111; Indels 22; Gaps 5;

Qy   28 AAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCTVTQVNLIQRHGARWPTSGARSRQVAA 87
              ||||||||||||||| : ||:||||||||:|:||||||||||||||: |:
Db   9 AAQLPIPAQXQXQXWSPYSPYFPVAXYXAPPAGCQIXQVNIIQRHGARFPTSGAATRIQAA 68

Qy   88 VAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRYSTLFEGGDVPF 147
              ||||||||| : ||| | | :||
Db   69 VAKLQSAXXXTDPKLDFLXNXTYXLGXDDLVPFGAXQSSQAGQEAFTRYSXLVSXDNLPF 128

Qy   148 VRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQVVLPEGNCTLCNNMCPNEVDGD-EST 206
              || ::||| ||||||||||:|:| : || ||| : :|||
Db   129 VRASGSDRVVDSATNWTAGFAXASXNTXPXLXVILSEXGNDTLDDNMCPXAGDSDPQXN 188

Qy   207 TWLGVFAPNITARLNAAAPSANLSDSDALTLMDMCPPDTLSSGNASPFCDLF--TAEEYV 264
              ||:| ||||: ||||||:| :|:| ||:|
Db   189 XWLAVFARPPITARLNAAAPGANLTDXDAXNLXXLCPFETVSXEXXSXFCDLFEXXPEEFX 248

Qy   265 SYEYYYDLDKYYGTGPGNALGPVQGVGVVNELLARLTGQAVRDETQTNRTLDSDPATFPL 324
              :|||| ||| || ||||||||||:|:|:|| :|||| : | :|||
Db   249 AFXYXGDDLDKFYGTGYGQPLGPVQGVGVGYINELLARLTXQAVRDNTQTNRTLDSSPXTFPL 308

Qy   325 NRTFYADFSHDNTMVPIFAALGLFNATA-LDPLKPDENRLWDSKLVPFSGHMTVEKLAC 383
              |||||||||||: ||||||||||||| |||| |||||||||:|||| |||: |||:
Db   309 NRTFYADFSHDNQMVAIFSAMGLFNQSAPLDPSXPDNRTWVTSKLVPFSARMVVERLXC 368

Qy   384 ------------SGKEAVRLVNDAVQPLEFCGG-VDGVCBLSAFVESQTYAREN 425
                          ||||:||||||||||||| |||:| | :|||:||:
Db   369 XXXGTXXXXXXXXXXXXXVRVLVNDAVQPLEFCCGGDXDGXCTLDAFVESQXYARED 428

Qy   426 GQGDFAKCGFVP 437
              ||:||:|| | |
Db   429 GQGDFEKCFATP 440

RESULT 11
US-08-993-359-26
; Sequence 26, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.

; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383,500-US
; CURRENT APPLICATION NUMBER: US/08/993,359A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 1480/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 1481/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 0301/97
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 0529/97
; EARLIER FILING DATE: 1997-05-07
; EARLIER APPLICATION NUMBER: 1388/97
; EARLIER FILING DATE: 1997-12-01
; EARLIER APPLICATION NUMBER: 60/046,082
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involutus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-08-993-359-26

Query Match   51.8%;   Score 1204; DB 3; Length 442;
Best Local Similarity 55.3%; Pred. No. 3.6e-125;
Matches 242; Conservative 51; Mismatches 139; Indels 6; Gaps 5;

Qy   1 MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGC 60
             |:   :|| | |||||||||||||||||| ||||:||
Db   1 MLFGFVALACLLSLSEVLATSVPKN-TAPTFPIPESEQRNWSPYSPYFPLAEYXAPPAGC 59

Qy   61 TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
             :|: ||:||||||||||:| | ||| || : :||||: | | | :
Db   60 QINQVNIIQRHGARFPTSGATTRIKAGLTKLQGVQNFTDAKFNFIKSFKYDLGNSDLVPF 119

Qy   121 GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQ 180
             ||| || | :|||||||| | |:||| ||| ||||| ||||||| |||:|
Db   120 GAAQSFDAGQEAFARYSKLVSKNNLPFIRADGSDRVVDSATNWTAGFASASHNTVQPKLN 179

Qy   181 VVLQEEGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMD 239
             || |||| || | ||| | :|||||| |||: :|||||||||:|:| ||:|
Db   180 LILPQTGNDTLEDNMCPAAGDSDPQVNAWLAVAFPSITARLNAAAAPSVNLTDTDAFNLVS 239

Qy   240 MCPPDTLSSGNASPFCDLFTA--EEYVSVEYYYDLDKYYGTGPNALGPVQGVGVVNELI 297
             :||| |:| ||||||| | ||||:| ||||||| || | ||||||||||:|:|
Db   240 LCAFLTVSKEKKSDFCTLFEGIPGSFEAFAYGGDLDKFYGTGYGQELGPVQGVGVVNELI 299

Qy   298 ARLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPL 356
             ||||:||||:|||||||||| |||||||||||||||||: ||||||||||||| |||
Db   300 ARLTNSAVRDNTQTNRTLDASPVTFPLNKTFYADFSHDNLMVAVFSAMGLFRQPAPLSTS 359

Qy   357 KPDENRLWDSKLVPFSGHMTVEKLACSGKEAVRLVNDAVQPLEFCGG--VDGVCELSAF 415
             |||||||||:|||| |||: |||:| ||||:|||||||||||||||| |||:| |:
Db   360 VPNPWRTWRTSSLVPFSGRMVVERLSCFGTTKVRVLVQDQVQPLEFCGGDRNGLCTLAKF 419

Qy   416 VESQTYARENGQGDFAKC 433
             |||:|||| ||:||| |
Db   420 VESQTFARSDGAGDFEKC 437

RESULT 12
US-09-482-558A-26
; Sequence 26, Application US/09482558A
; Patent No. 6569659
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens

```
;  APPLICANT: Fuglsang, Claus C.
;  APPLICANT: Ostergaard, Peter R.
;  TITLE OF INVENTION: Phytase Polypeptides
;  FILE REFERENCE: 5383.500-US
;  CURRENT APPLICATION NUMBER: US/09/482,558A
;  CURRENT FILING DATE: 2000-01-13
;  PRIOR APPLICATION NUMBER: US/08/993,359
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 1480/96
;  PRIOR FILING DATE: 1996-12-20
;  PRIOR APPLICATION NUMBER: 1481/96
;  PRIOR FILING DATE: 1996-12-20
;  PRIOR APPLICATION NUMBER: 0301/97
;  PRIOR FILING DATE: 1997-03-18
;  PRIOR APPLICATION NUMBER: 0529/97
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 1388/97
;  PRIOR FILING DATE: 1997-12-01
;  PRIOR APPLICATION NUMBER: 60/046,082
;  PRIOR FILING DATE: 1997-05-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 26
;  LENGTH: 442
;  TYPE: PRT
;  ORGANISM: Paxillus involtus
;  FEATURE:
;  NAME/KEY: SIGNAL
;  LOCATION: (1)...(19)
US-09-482-558A-26

Query Match            51.8%;       Score 1204; DB 4; Length 442;
Best Local Similarity  55.3%;       Pred. No. 3.6e-125;
Matches  242; Conservative  51; Mismatches 139; Indels 6; Gaps 5;

Qy   1  MVSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFPVEPYAAPPEGC    60
Db   1  MLFGFVALACLLSLSEVLATSVPKN-TAPTFPIPESEQRNWSPYFPPLAEYKAPPAGC    59

Qy  61  TVTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF  120
Db  60  QINQVNIIQRHGARPFTSGATTRIKAGLTKLQGVQNFTDAKFNFIKSFKYDLGNSDLVPF  119

Qy 121  GANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGEIVLPTLQ  180
Db 120  GAAQSPDAGQEAFARYSKLVSKNNLPFFIRADGSDRVVDSATNWTAGFASASHNTVQPKLN 179

Qy 181  VVLQEBGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSVNLTDTDAFNLVS  239
Db 180  LILPQTGNDTLEDNMCPAAGDSDPQVNAWLAVAFPSITARLNAAAPSVNLTDTDAFNLVS  239

Qy 240  MCPFDTLSSGNASPPCDLFTA--EEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELL   297
Db 240  LCAFLTVSKEKKSDFCTLFEGIPGSFEAFAYGGDLDKFYGTGYGQELGPVQGVGYVNELI  299

Qy 298  ARLTGQAVRDETQTNRTLDSDPATPPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPL  356
Db 300  ARLTNSAVRDNTQTNRTLDASPVTFPLNKTFYADFSHDNLMVAVFSAMGLFRQPAPLSTS  359

Qy 357  KPDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAF  415
Db 360  VPNPWRTWRTSSLVPFSGRMVVERLSCFGTTKVRVLVQDQVQPLEFCGGDRNGLCTILAKF 419

Qy 416  VESQTYARENGQGDFAKC  433
Db 420  VESQTFARSDGAGDFEKC  437

RESULT 13
US-08-993-359-28
; Sequence 28, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:
```

```
;  APPLICANT: Lassen, Soren F.
;  APPLICANT: Bech, Lisbeth
;  APPLICANT: Ohmann, Anders
;  APPLICANT: Breinholt, Jens
;  APPLICANT: Fuglsang, Claus C.
;  APPLICANT: Ostergaard, Peter R.
;  TITLE OF INVENTION: Phytase Polypeptides
;  FILE REFERENCE: 5383.500-US
;  CURRENT APPLICATION NUMBER: US/08/993,359A
;  CURRENT FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 1480/96
;  EARLIER FILING DATE: 1996-12-20
;  EARLIER APPLICATION NUMBER: 1481/96
;  EARLIER FILING DATE: 1996-12-20
;  EARLIER APPLICATION NUMBER: 0301/97
;  EARLIER FILING DATE: 1997-03-18
;  EARLIER APPLICATION NUMBER: 0529/97
;  EARLIER FILING DATE: 1997-05-07
;  EARLIER APPLICATION NUMBER: 1388/97
;  EARLIER FILING DATE: 1997-12-01
;  EARLIER APPLICATION NUMBER: 60/046,082
;  EARLIER FILING DATE: 1997-05-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 28
;  LENGTH: 442
;  TYPE: PRT
;  ORGANISM: Paxillus involtus
;  FEATURE:
;  NAME/KEY: SIGNAL
;  LOCATION: (1)...(19)
US-08-993-359-28

Query Match            51.7%;       Score 1202; DB 3; Length 442;
Best Local Similarity  52.6%;       Pred. No. 6e-125;
Matches  230; Conservative  61; Mismatches 128; Indels 18; Gaps 5;

Qy   2  VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFPVEPYAAPPEGCT   61
Db  14  LSEVFAASVPRN---------IAPKFSIPESEQRNWSPYSPYFPPLAEYKAPPAGCE    60

Qy  62  VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG  121
Db  61  INQVNIIQRHGARPFTSGAATRIKAGLSKLQSVQNFTDPKPDFIKSFTYDLGTSDLVPFG  120

Qy 122  ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV  181
Db 121  AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL  180

Qy 182  VLQEBGNCTLCNNMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM  240
Db 181  ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFPSVTAQLNAAAPGANLTDADAFNLVSL  240

Qy 241  CPFDTLSSGNASPPCDLFTA--EEYVSYEYYDLDKYYGTGPGNALGPVQGVGYVNELLA  298
Db 241  CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTGYGQALGPVQGVGYVNELLA 300

Qy 299  RLTGQAVRDETQTNRTLDSDPATPPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK  357
Db 301  RLTNSAVNDNTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST  360

Qy 358  PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG-VDGVCELSAFV  416
Db 361  PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRVLVQDQVQPLEFCGGDQDGLCALDKFV  420

Qy 417  ESQTYARENGQGDFAKC  433
Db 421  ESQAYARSGGAGDFEKC  437

RESULT 14
US-09-273-871A-4
; Sequence 4, Application US/09273871A
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; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involtus
US-09-273-871A-4

Query Match   51.7%;   Score 1202;   DB 4; Length 442;
Best Local Similarity 52.6%;   Pred. No. 6e-125;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps   5;

```
Qy      2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT  61
          :|:|:.|||         .|::|:.|||:.|:||:
Db     14 LSEVFAASVPRN---------IAPKFSIPESEQRNWSPYSPYFFPLAEYKAPPAGCE  60

Qy     62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
          :.|||||||||||.||   |:.||||.|:.:..|:||.|:|:||.:|||.::||||||||
Db     61 INQVNIIQRHGARFPTSGAATRIKAGLSKLQSVQNFTDPKFDFIKSFTYDLGTSDLVPFG 120

Qy    122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
          |.|:| : |.|   ||||||||.||||.||.|..:.:.||:|||...
Db    121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL 180

Qy    182 VLQEEGNCTLCNMMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||.||||.|| :||||  |.|:||||.|:.: ||:||||.:.:...::
Db    181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFFSVTAQLNAAAPGANLTDADAFNLVSL 240

Qy    241 CPFDTLSSGNASPFCDLFTA--EBYVSYEYYYDLDKYYGTGPGNALGPVQGVGVYNELLA 298
          ||| ||  || |  |||.|   |:||||||:|||||||..|||||||||||||||||||.
Db    241 CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTYGQALGPVQGVGVYINELLA 300

Qy    299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
          |||.:|.|.:||.|||||..||.|||| ||||||||||.|...: :::| :|
Db    301 RLTNSAVNDNTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360

Qy    358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG--VDGVCELSAFV 416
          ||:||||.|:.||.||:   ::|.  |:|||||||:.|||||||:|||     ||.|.|||
Db    361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRVLVQDQVQPLEFCGGDQDGLCALDKFV 420

Qy    417 ESQTYARENGQGDFAKC 433
          |||.|||..|:|||.||
Db    421 ESQAYARSGGAGDFEKC 437
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RESULT 15
US-09-482-558A-28
; Sequence 28, Application US/09482558A
; Patent No. 6569659
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens

; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/482,558A
; CURRENT FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: US/08/993,359
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 1480/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 1481/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involtus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-482-558A-28

Query Match   51.7%;   Score 1202;   DB 4; Length 442;
Best Local Similarity 52.6%;   Pred. No. 6e-125;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps   5;

```
Qy      2 VSSAFAPSILLSLMSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFPVEPYAAPPEGCT  61
          :|:|:.|||         .|::|:.|||:.|:||:
Db     14 LSEVFAASVPRN---------IAPKFSIPESEQRNWSPYSPYFFPLAEYKAPPAGCE  60

Qy     62 VTQVNLIQRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFG 121
          :.|||||||||||.||   |:.||||.|:.:..|:||.|:|:||.:|||.::||||||||
Db     61 INQVNIIQRHGARFPTSGAATRIKAGLSKLQSVQNFTDPKFDFIKSFTYDLGTSDLVPFG 120

Qy    122 ANQSHQTGTDMYTRYSTLFEGGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLPTLQV 181
          |.|:| : |.|   ||||||||.||||.||.|..:.:.||:|||...
Db    121 AAQSFDAGLEVFARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASASRNAIQPKLDL 180

Qy    182 VLQEEGNCTLCNMMCPNEVDGD-ESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDM 240
          ||||||||.||||.|| :||||  |.|:||||.|:.: ||:||||.:.:...::
Db    181 ILPQTGNDTLEDNMCPAAGESDPQVDAWLASAFFSVTAQLNAAAPGANLTDADAFNLVSL 240

Qy    241 CPFDTLSSGNASPFCDLFTA--EBYVSYEYYYDLDKYYGTGPGNALGPVQGVGVYNELLA 298
          ||| ||  || |  |||.|   |:||||||:|||||||..|||||||||||||||||||.
Db    241 CPFMTVSKEQKSDFCTLFEGIPGSFEAFAYAGDLDKFYGTYGQALGPVQGVGVYINELLA 300

Qy    299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMVPIFAALGLFNATA-LDPLK 357
          |||.:|.|.:||.|||||..||.|||| ||||||||||.|...: :::| :|
Db    301 RLTNSAVNDNTQTNRTLDAAPDTFPLNKTMYADFSHDNLMVAVFSAMGLFRQSAPLSTST 360

Qy    358 PDENRLWVDSKLVPFSGHMTVEKLACSGKEAVRVLVNDAVQPLEFCGG--VDGVCELSAFV 416
          ||:||||.|:.||.||:   ::|.  |:|||||||:.|||||||:|||     ||.|.|||
Db    361 PDPNRTWLTSSVVPFSARMAVERLSCAGTTKVRVLVQDQVQPLEFCGGDQDGLCALDKFV 420

Qy    417 ESQTYARENGQGDFAKC 433
          |||.|||..|:|||.||
Db    421 ESQAYARSGGAGDFEKC 437
```

Search completed: May 27, 2005, 08:34:00
Job time : 45 secs